

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 04:37:24 ; Search time 1703.81 Seconds  
(without alignments)  
7460.491 Million cell updates/sec

Title: US-09-852-261-5  
Perfect score: 523  
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaaccattc 523

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	364.8	69.8	558	9	AI503976	AI503976 vm43d08.x
c	2	363	69.4	623	9	AW146128	AW146128 um37e10.x
c	3	348.2	66.6	549	9	AI169253	AI169253 EST215088
c	4	347	66.3	558	9	AI265629	AI265629 uj04b07.x
	5	339.6	64.9	614	14	CD373004	CD373004 UI-R-GR0-
	6	339.2	64.9	816	9	AI119218	AI119218 ue94h02.y
	7	334.8	64.0	594	10	BF383724	BF383724 602044632
	8	334.4	63.9	796	14	CB959991	CB959991 AGENCOURT
c	9	322.2	61.6	499	9	AW495481	AW495481 UI-M-BH3-
c	10	320.8	61.3	642	9	AI876493	AI876493 uj59b10.x
c	11	320.8	61.3	673	12	BM984670	BM984670 UI-CF-EC1
c	12	316.8	60.6	575	9	AI248089	AI248089 qh69f05.x
c	13	309.2	59.1	468	9	AI169770	AI169770 EST215669
c	14	305	58.3	498	9	AA542914	AA542914 ni98c10.s
	15	299	57.2	882	9	AI604642	AI604642 vm43d08.y
c	16	296.4	56.7	653	13	BQ200567	BQ200567 UI-R-DZ1-
c	17	291.6	55.8	527	9	AA913900	AA913900 ol35g05.s
c	18	271.6	51.9	521	9	AW493459	AW493459 UI-M-BH3-
	19	271.6	51.9	559	12	BI715603	BI715603 ic34h10.y
	20	271.6	51.9	602	13	BU590710	BU590710 AGENCOURT
	21	271.6	51.9	621	12	BI221656	BI221656 602936980
	22	271.6	51.9	1658	11	AK081019	AK081019 Mus muscu
c	23	270.6	51.7	595	9	AI573421	AI573421 mo04b11.x
c	24	270	51.6	499	12	BI676839	BI676839 ic56a08.x
c	25	266.8	51.0	500	9	AA945553	AA945553 EST201052
c	26	266.8	51.0	525	9	AA963258	AA963258 UI-R-E1-g
	27	266	50.9	665	9	AA690767	AA690767 vu57d12.r
	28	265.2	50.7	559	12	BI715465	BI715465 ic33b09.y
	29	263.8	50.4	799	9	AI314558	AI314558 uj48d07.y
c	30	263.6	50.4	525	9	AI599751	AI599751 EST251454
c	31	261.4	50.0	499	12	BI294072	BI294072 UI-R-DK0-
c	32	260.4	49.8	561	12	BI714874	BI714874 ic33b09.x
c	33	258.4	49.4	502	9	AI104669	AI104669 EST213958
c	34	258	49.3	564	12	BI714981	BI714981 ic34h10.x
	35	256	48.9	2170	11	AK038119	AK038119 Mus muscu
c	36	254.8	48.7	430	9	AI478804	AI478804 tm52e04.x
	37	254.8	48.7	558	12	BI715475	BI715475 ic33c08.y
	38	250.8	48.0	512	9	AI876203	AI876203 uj59b10.y
	39	249.6	47.7	949	14	CB589117	CB589117 AGENCOURT
c	40	248.2	47.5	637	9	AW413016	AW413016 uq49h08.x
	41	246.4	47.1	473	9	AA451360	AA451360 vf84g03.r
c	42	246.4	47.1	486	9	AA993659	AA993659 ot85g11.s
	43	246.2	47.1	773	12	BI144500	BI144500 602908689
	44	243.2	46.5	482	9	AA456717	AA456717 aa13h06.r
c	45	243	46.5	474	9	AI526955	AI526955 uj48d07.x

# ALIGNMENTS

## RESULT 1

AI503976/c

LOCUS AI503976 558 bp mRNA linear EST 11-MAR-1999

DEFINITION vm43d08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI503976

VERSION AI503976.1 GI:4401827

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 558)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:565223

This clone was previously sequenced on the 5' end only, this new data is from the 3' end

High quality sequence stop: 440.

## FEATURES

source

Location/Qualifiers

1. .558

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:1001007"

/tissue\_type="diaphragm"

/dev\_stage="adult"

/lab\_host="SOLR (kanamycin resistant)"

/clone\_lib="Stratagene mouse diaphragm (#937303)"

/note="Organ: diaphragm; Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor

sequence: 5' GAATTCGGCACCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

BASE COUNT

103 a 133 c 149 g 173 t

ORIGIN

Query Match 69.8%; Score 364.8; DB 9; Length 558;  
 Best Local Similarity 83.2%; Pred. No. 8.8e-81;  
 Matches 441; Conservative 0; Mismatches 82; Indels 7; Gaps 2;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      530 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 471

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      470 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCTCAG 411

Qy      121 ACAGGCATCGTGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      410 ACAGGCATTGTGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 351

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      350 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCAGCGCCACACTGAC 291

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||| ||||| ||||| || || || || || || || || || || || || || || || ||
Db      290 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 231

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      230 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 171

Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      ||| ||||| || || || || || || || || || || || || || || || ||
Db      170 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 111

Qy      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
      || || || || || || || || || || || || || || || || || || || ||
Db      110 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAAAGTCCAATA 51

Qy      475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      50 ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATTTC 1
  
```

## RESULT 2

AW146128/c

LOCUS AW146128 623 bp mRNA linear EST 10-OCT-2000

DEFINITION um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone  
 IMAGE:2247498 3' similar to gb:X04482 Mouse mRNA for  
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AW146128

VERSION AW146128.1 GI:6167864

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 623)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person

```

TITLE      The WashU-NCI Mouse EST Project 1999
JOURNAL    Unpublished
COMMENT    Contact: Marra M/WashU-NCI Mouse EST Project 1999
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: mouseest@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           MGI:1006958
           Seq primer: custom primer used
           High quality sequence stop: 499.

FEATURES   Location/Qualifiers
            source                1. .623
                                   /organism="Mus musculus"
                                   /mol_type="mRNA"
                                   /strain="C57BL"
                                   /db_xref="taxon:10090"
                                   /clone="IMAGE:2247498"
                                   /dev_stage="embryo, 14 dpc"
                                   /lab_host="DH10B"
                                   /clone_lib="Sugano mouse embryo mewa"
                                   /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                                   Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                                   with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT];
                                   double-stranded cDNA was ligated to a DraIII adaptor
                                   [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                                   sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                                   CACCATGTG). XhoI should be used to isolate the cDNA
                                   insert. Size selection was performed to exclude fragments
                                   <1.5kb. Library constructed by Dr. Sumio Sugano
                                   (University of Tokyo Institute of Medical Science).
                                   Custom primers for sequencing: 5' end primer
                                   CTTCTGCTCTAAAAGCTGCG and 3' end primer
                                   CGACCTGCAGCTCGAGCACA."

BASE COUNT      123 a      138 c      170 g      191 t      1 others
ORIGIN

```

Query Match 69.4%; Score 363; DB 9; Length 623;  
Best Local Similarity 81.9%; Pred. No. 2.5e-80;  
Matches 433; Conservative 0; Mismatches 90; Indels 6; Gaps 1;

[illegible]



/mol\_type="mRNA"  
 /db\_xref="taxon:10118"  
 /clone="RKIBP33"  
 /clone\_lib="Normalized rat kidney, Bento Soares"  
 /note="Organ: kidney; Vector: pT7T3Pac; Site\_1: EcoRI;  
 Site\_2: NotI"

BASE COUNT      112 a      140 c      133 g      164 t  
 ORIGIN

Query Match                      66.6%;    Score 348.2;    DB 9;    Length 549;  
 Best Local Similarity    81.8%;    Pred. No. 1.3e-76;  
 Matches 428;    Conservative    0;    Mismatches 88;    Indels    7;    Gaps    2;

```

Qy      8 AGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCT 67
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     549 AGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCTGTGTGGACCAAGGGGCT 490

Qy     68 TTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCA 127
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     489 TTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTCTGAAGGGCACCACAGACGGGCA 430

Qy    128 TCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCAC 187
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    429 TTGTGGATGAGTGTAGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCTC 370

Qy    188 CCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCA 247
      | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    369 CGCTGAAGCCTACAAAGTCAGCTCGTTCATCCGGGCCCAGCGCCACATTGACATGCCCA 310

Qy    248 AGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGA 307
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    309 AGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGGA 250

Qy    308 AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATG 367
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    249 AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACTTACAGAATG 190

Qy    368 TAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCA 427
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    189 TAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCTTG 130

Qy    428 CAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCACATTTTC 481
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    129 AGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTTTC 70

Qy    482 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     69 AGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 27
  
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RESULT 4  
 AI265629/c  
 LOCUS      AI265629                      558 bp      mRNA      linear      EST 18-NOV-1998  
 DEFINITION    uj04b07.x1 Sugano mouse liver mlia Mus musculus cDNA clone  
               IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for  
               preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.  
 ACCESSION    AI265629

VERSION AI265629.1 GI:3883787  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 558)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.  
 TITLE The WashU-HHMI Mouse EST Project  
 JOURNAL Unpublished  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of MedicineP  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:975225  
 Seq primer: custom primer used  
 High quality sequence stop: 495.  
 FEATURES Location/Qualifiers  
 source 1. 558  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1890901"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="Sugano mouse liver mlia"  
 /note="Organ: liver; Vector: pME18S-FL3; Site\_1: DraIII  
 (CACTGTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA  
 was primed with an oligo(dT) primer  
 [ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was  
 ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested  
 and cloned into distinct DraIII sites of the pME18S-FL3  
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should  
 be used to isolate the cDNA insert. Size selection was  
 performed to exclude fragments <1.5kb. Library  
 constructed by Dr. Sumio Sugano (University of Tokyo  
 Institute of Medical Science). Custom primers for  
 sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end  
 primer CGACCTGCAGCTCGAGCACA."  
 BASE COUNT 106 a 135 c 156 g 161 t  
 ORIGIN

Query Match 66.3%; Score 347; DB 9; Length 558;  
 Best Local Similarity 82.0%; Pred. No. 2.5e-76;  
 Matches 414; Conservative 0; Mismatches 85; Indels 6; Gaps 1;



[illegible]

CD373004

LOCUS CD373004 614 bp mRNA linear EST 29-MAY-2003

DEFINITION UI-R-GR0-csv-j-17-0-UI.r1 UI-R-GR0 *Rattus norvegicus* cDNA clone  
UI-R-GR0-csv-j-17-0-UI 5', mRNA sequence.

ACCESSION CD373004

VERSION CD373004.1 GI:31157094

KEYWORDS EST.

SOURCE      Rattus norvegicus (Norway rat)

ORGANISM *Rattus norvegicus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 614)

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE      Normalization and subtraction: two approaches to facilitate gene  
             discovery

JOURNAL     Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT      Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: James Lin, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/rat.html>  
 Seq primer: M13 REVERSE.

FEATURES      Location/Qualifiers  
                 source      1. .614  
                                 /organism="Rattus norvegicus"  
                                 /mol\_type="mRNA"  
                                 /strain="Sprague-Dawley"  
                                 /db\_xref="taxon:10116"  
                                 /clone="UI-R-GR0-csv-j-17-0-UI"  
                                 /tissue\_type="Whole embryo"  
                                 /dev\_stage="embryo 13dpc"  
                                 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
                                 /clone\_lib="UI-R-GR0"  
                                 /note="Vector: pYX-Asc; Site\_1: EcoR I; Site\_2: Not I;  
                                 UI-R-GR0 is a cDNA library containing the following  
                                 tissue(s): rat whole embryo 13dpc. The library was  
                                 constructed according to Bonaldo, Lennon and Soares,  
                                 Genome Research, 6:791-806, 1996. Denatured RNA was size  
                                 fractionated on a 1% agarose gel. First strand cDNA  
                                 synthesis was primed with oligo-dT primer containing a Not  
                                 I site. Double strand cDNA was size selected according to  
                                 mRNA size fraction, ligated with EcoR I adaptor, digested  
                                 with NotI and then cloned directionally into pYX-Asc  
                                 vector. The library tag sequence located between the Not I  
                                 site and the polyA tail is CATCTCTACT. This library was  
                                 created for the University of Iowa Program for Rat Gene  
                                 Discovery and Mapping (Val Sheffield, Bento Soares and Tom  
                                 Casavant)."

BASE COUNT      171 a      168 c      154 g      119 t      2 others  
 ORIGIN

Query Match      64.9%;    Score 339.6;    DB 14;    Length 614;  
 Best Local Similarity    81.4%;    Pred. No. 1.9e-74;  
 Matches 393;    Conservative    0;    Mismatches    90;    Indels    0;    Gaps    0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      116 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 175

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      176 AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACACAG 235

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



Seq primer: custom primer used  
High quality sequence stop: 473.

BASE COUNT	230 a	219 c	172 g	187 t	8 others
ORIGIN					

Query Match 64.9%; Score 339.2; DB 9; Length 816;  
Best Local Similarity 81.2%; Pred. No. 2.5e-74;  
Matches 389; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy		1 GGACCGGAGACGCTCTGCCGTGCTGAGCTGGTGGATGCTCCTTCAGTTCCGTGTGTGGAGAC	60
Db	323	GGACCAGAGACCCCTTTGC GGGGCTGAGCTGGTGGATGCTCCTTCAGTTCCGTGTGTGGACCG	382
Qy		61 AGGGGCTTTTTATTTC AACAAGCCCACAGGATA CGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	383	AGGGGCTTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG	442
Qy		121 ACAGGCATCGTGGA TGAGTGCTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	443	ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	502
Qy		181 TGTGCACCCCTCAAG CCGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Db	503	TGTGCCCCACTGAAG CCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCAACTGAC	562
Qy		241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAAATGAAGTCTCAGAGG	300
Db	563	ATGCCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAAACGAAGCTGCAAAGG	622
Qy		301 AGAAGGAAAGGAAGTA CATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	623	AGAAGGAAAGGAAGTA CATTTGAAGAACACAAGTAGAGGAAGTGCANGAAACAAGACCTA	682

Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420  
 ||| ||||| || || ||| | |||| | | ||| ||||| || |||||  
 Db 683 CAGAATGTANGAGGAGCCTNCCACGGAGCAGAANATGCCACATCACCGCANGATCCTTTG 742  
 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATT 479  
 || | ||||| || ||| ||||| ||| ||| ||| ||| |||  
 Db 743 CTGCTTGAGCAACCTGCANAACATCGAAACACCTACCAAATAACATNTATAAGTCCAAT 801

# RESULT 7

BF383724

LOCUS BF383724 594 bp mRNA linear EST 27-NOV-2000

DEFINITION 602044632F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:4194295 5', mRNA sequence.

ACCESSION BF383724

VERSION BF383724.1 GI:11365029

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 594)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9527 row: p column: 08

High quality sequence stop: 589.

## FEATURES

source

Location/Qualifiers

1..594

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:4194295"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI\_CGAP\_Li9"

/note="Organ: liver; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 175 a 162 c 142 g 115 t

## ORIGIN

Query Match 64.0%; Score 334.8; DB 10; Length 594;

Best Local Similarity 82.0%; Pred. No. 2.9e-73;

Matches 400; Conservative 0; Mismatches 82; Indels 6; Gaps 1;

Qy 16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTTC 75



cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: NDAM371 row: p column: 18  
 High quality sequence stop: 707.

FEATURES  
 source Location/Qualifiers  
 1. .796  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30341081"  
 /tissue\_type="Human Placenta"  
 /lab\_host="DH10B TonA"  
 /clone\_lib="NIH\_MGC\_147"  
 /note="Organ: placenta; Vector: pBluescriptR; Site\_1:  
 all-XhoI; Site\_2: BamH; Oligo-dT primed using primer  
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
 insert size 2.3 kb and normalized to ROT 5. This is a  
 primary library enriched for full-length clones and  
 constructed using the Cap-trapper method (Carninci, in  
 preparation). Library constructed by M. Brownstein  
 (NIMH/NHGRI, National Institutes of Health). Note: This is  
 a NIH\_MGC library."

BASE COUNT 224 a 197 c 191 g 184 t  
 ORIGIN

Query Match 63.9%; Score 334.4; DB 14; Length 796;  
 Best Local Similarity 84.6%; Pred. No. 3.9e-73;  
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      180 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 239
      |||

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      |||
Db      240 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 299
      |||

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      300 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 359
      |||

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      360 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 419
      |||

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      420 ATGCCCAAGACCCAG----- 434
      |||

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      435 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 487
      |||

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||

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Db      488 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 547
Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
Db      548 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 607
Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
Db      608 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 653

```

# RESULT 9

AW495481/c

LOCUS AW495481 499 bp mRNA linear EST 24-FEB-2000

DEFINITION UI-M-BH3-ay-g-11-0-UI.s1 NIH\_BMAP\_M\_S4 Mus musculus cDNA clone  
UI-M-BH3-ay-g-11-0-UI 3', mRNA sequence.

ACCESSION AW495481

VERSION AW495481.1 GI:7065762

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 499)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NotI site  
and the oligo-dT track served to identify it as a clone from the  
normalized pineal glands library cDNA Library Preparation: M.B.  
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA  
clones from RESEARCH GENETICS. It should be noted that Bento Soares  
is generating a small number of additional specialized  
non-redundant arrays of BMAP cDNAs whose availability will be  
considered under appropriate and limited collaborative arrangements  
Seq primer: M13 Forward  
POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1. .499

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"



```

/clone="UI-M-BH3-auy-g-11-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_M_S4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (LifeTechnologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=NIH_BMAP_M_S4
TAG_TISSUE=pineal-glands
TAG_SEQ=CAGAC"

```

```

BASE COUNT      86 a      112 c      124 g      177 t
ORIGIN

```

```

Query Match          61.6%; Score 322.2; DB 9; Length 499;
Best Local Similarity 82.3%; Pred. No. 4e-70;
Matches 396; Conservative 0; Mismatches 78; Indels 7; Gaps 2;

```

```

Qy      50 TGTGTGGAGACAGGGGCTTTTATTTCACAAAGCCACAGGATACGGCTCCAGCAGTCGGA 109
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      499 TGTGTGGACCGAGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGA 440

Qy      110 GGGCACCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGC 169
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      439 GGGCACCTCAGACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGAC 380

Qy      170 TGGAGATGTACTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGC 229
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      379 TGGAGATGTACTGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGC 320

Qy      230 GCCACACCGACATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGA 289
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      319 GCCCACTGACATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGA 260

Qy      290 AGTCTCAGAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGA 349

```

[illegible]



Db 83 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 24

QY 475 ACATTTCAAAGATGGCATTTCCTCC 497

Db 23 ACATTACAAAGATGGGCATTTCCTCC 1

RESULT 11

BM984670/c

LOCUS BM984670 673 bp mRNA linear EST 20-FEB-2003

DEFINITION UI-CF-EC1-abj-k-24-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone  
UI-CF-EC1-abj-k-24-0-UI 3', mRNA sequence.

ACCESSION BM984670

VERSION BM984670.1 GI:19610417

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 673)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..673

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-CF-EC1-abj-k-24-0-UI"

/tissue\_type="Lung"

/dev\_stage="Adult and Fetal"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-CF-EC1"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-CF-EC1 is a normalized cDNA library containing the  
following tissue(s): Normal lung from adult and from fetal  
day 64, day 87, week 19 and week 42. The library was

constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.

TAG\_LIB=UI-CF-EC1

TAG\_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383

TAG\_SEQ=AAGTGCTTAC"

BASE COUNT        152 a        164 c        169 g        188 t  
ORIGIN

Query Match                    61.3%;    Score 320.8;    DB 12;    Length 673;  
Best Local Similarity    84.2%;    Pred. No. 9.7e-70;  
Matches 443;    Conservative    0;    Mismatches 27;    Indels 56;    Gaps 5;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db     492 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 433

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     432 AGGGG-TTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 374

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db     373 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 314

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db     313 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 254

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db     253 ATGCCCAAGACCCAG----- 239

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db     238 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 186

Qy     361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db     185 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCTTTG 126

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db     125 CTCTGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 66

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db      65 TTAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 20

```

RESULT 12  
AI248089/c  
LOCUS AI248089 575 bp mRNA linear EST 01-DEC-1998  
DEFINITION qh69f05.x1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA  
clone IMAGE:1849953 3' similar to gb:X57025\_rnal INSULIN-LIKE  
GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.  
ACCESSION AI248089  
VERSION AI248089.1 GI:3843486  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 575)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 918 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 380.  
FEATURES  
source Location/Qualifiers  
1..575  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1849953"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares\_fetal\_liver\_spleen\_1NFLS\_S1"  
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)  
with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;  
This is a subtracted version of the original Soares fetal  
liver spleen 1NFLS library. 1st strand cDNA was primed  
with a Pac I - oligo(dT) primer [5'  
AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo."  
BASE COUNT 135 a 152 c 131 g 156 t 1 others  
ORIGIN

Query Match 60.6%; Score 316.8; DB 9; Length 575;  
Best Local Similarity 83.8%; Pred. No. 9.4e-69;  
Matches 428; Conservative 0; Mismatches 28; Indels 55; Gaps 4;

Qy 16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTTC 75  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 551 TGCGGGGCTGAGCTGGTGNATGCTCTTCAGTTCGTGTGTGAAGACAGGGGCTTTTATTTTC 492



Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org  
Seq primer: M13-21.

FEATURES                      Location/Qualifiers  
    source                      1. .468  
                                /organism="Rattus sp."  
                                /mol\_type="mRNA"  
                                /db\_xref="ATCC (inhost):2027570"  
                                /db\_xref="taxon:10118"  
                                /clone="RLIAT07"  
                                /clone\_lib="Normalized rat liver, Bento Soares"  
                                /note="Organ: liver; Vector: pT7T3Pac; Site\_1: EcoRI;  
                                Site\_2: NotI"

BASE COUNT                      85 a       115 c       119 g       149 t  
ORIGIN

Query Match                      59.1%;    Score 309.2;    DB 9;    Length 468;  
Best Local Similarity              81.8%;    Pred. No. 7.2e-67;  
Matches 383;    Conservative       0;    Mismatches 78;    Indels       7;    Gaps       2;

```
Qy      63 GGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGAC 122
      |||
Db      468 GGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCACAGAC 409

Qy      123 AGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTG 182
      |||
Db      408 GGGCATTGTGGATGAGTGTGCTCCCGGAGCTGTGATCTGAGGAGGTTGGAGATGTACTG 349

Qy      183 TGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACAT 242
      |||
Db      348 TGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCAGCGCCACACTGACAT 289

Qy      243 GCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAG 302
      |||
Db      288 GCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAG 229

Qy      303 AAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTACA 362
      |||
Db      228 AAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGAGGAAACAAGACCTACA 169

Qy      363 GGATGTAGGAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCT 422
      |||
Db      168 GAATGTAGGAGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCT 109

Qy      423 CTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCAC 476
      |||
Db      108 GCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACC 49

Qy      477 ATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db      48 ATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 1
```

RESULT 14  
AA542914/c  
LOCUS                      AA542914                      :                      498 bp                      mRNA                      linear                      EST 19-AUG-1997



Qy 60 CAGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCA 119  
 |||  
 Db 416 CAGGGGC-TTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCA 358  
 Qy 120 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTA 179  
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 Db 357 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTA 298  
 Qy 180 CTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGA 239  
 ||  
 Db 297 TTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGA 238  
 Qy 240 CATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAG 299  
 |||  
 Db 237 CATGCCCAAGACCCAG----- 222  
 Qy 300 GAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACT 359  
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 Db 221 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACT 170  
 Qy 360 ACAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTT 419  
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 Db 169 ACAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTT 110  
 Qy 420 GCTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACA 477  
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 Db 109 GCTCTGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACA 50  
 Qy 478 TTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523  
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 Db 49 TTTAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 3

# RESULT 15

AI604642

LOCUS AI604642 882 bp mRNA linear EST 21-APR-1999

DEFINITION vm43d08.y1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1001007 5' similar to gb:M11568 INSULIN-LIKE GROWTH FACTOR IB PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI604642

VERSION AI604642.1 GI:4613809

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 882)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine

DEFINITION ni98c10.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone IMAGE:984882 3' similar to gb:X57025\_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA542914

VERSION AA542914.1 GI:2291394

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 498)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 603 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 412.

FEATURES

source Location/Qualifiers

1..498

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:984882"

/sex="male"

/tissue\_type="normal prostate"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Pr21"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 105 a 135 c 123 g 135 t

ORIGIN

Query Match 58.3%; Score 305; DB 9; Length 498;

Best Local Similarity 83.5%; Pred. No. 8.2e-66;

Matches 440; Conservative 0; Mismatches 30; Indels 57; Gaps 6;

Qy 1 GGACCGGAGACGCTCTGCGGTGC-TGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 59

|||||||

Db 476 GGACCGGAGAACTTTGCGGGGCTTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 417

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:565223

This read is a RESEQUENCE of a previously sequenced mouse clone

This read has been verified (found to hit its original self in the  
correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 361.

#### FEATURES

source

Location/Qualifiers

1. .882

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:1001007"

/tissue\_type="diaphragm"

/dev\_stage="adult"

/lab\_host="SOLR (kanamycin resistant)"

/clone\_lib="Stratagene mouse diaphragm (#937303)"

/note="Organ: diaphragm; Vector: pBluescript SK-; Site\_1:

EcoRI; Site\_2: XhoI; Cloned unidirectionally from mRNA

prepared from diaphragm muscle. Primer: Oligo dT. Average

insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor

sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'

CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

#### BASE COUNT

236 a 226 c 183 g 223 t 14 others

#### ORIGIN

Query Match 57.2%; Score 299; DB 9; Length 882;

Best Local Similarity 77.2%; Pred. No. 3e-64;

Matches 393; Conservative 0; Mismatches 109; Indels 7; Gaps 3;

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Db      377 GGACCAGAGACCCTTTGCGGNGCTGAGCTGNTGGATGCTCTTCAGTTCGTGTGTGGACCG 436

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      437 AGGGGCTTTTACTTCAACAAGCCCAAGGCTATGGCTCCAGCATTTTCGAGGGCACCTCAG 496

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      497 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGANGAGACTGGAGATGTAC 556

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      557 TGTGCCCCACTGAAGCCTACANAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 616

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      617 ATGCNNCAGACTCAGAAGTCCCCGTNCCTATCGACNNAACAGAAAACGAAGCTTGCAAGG 676

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAATA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 677 GAGAGGGAAGGGAGTACATTTGAGGAACACANGTNGAGGAAGTGCANGAAACAAGACCTA 736  
 Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420  
 | ||||| || || ||||| | | |||| || || ||||  
 Db 737 CCAGATGTANGAGGAGCCTTC--AACCGAGCAGAAATGCACATCACCCGNAGATCCTTTG 794  
 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAA---AAAATAAGTTTGATCAC 476  
 || || || || ||||| | | || || || || || ||  
 Db 795 CT-GCTTGAGCTAACTGCAAACATCGAACCCTTACCAATTACAATAATAAGTTCAATAA 853  
 Qy 477 ATTTCAAAGATGGCATTTCCTCCCAATGAA 505  
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 Db 854 CATACAAAGATGGCATTTCCTCCCAATGAA 882

Search completed: December 13, 2003, 07:29:51  
 Job time : 1704.81 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 05:41:20 ; Search time 2336.77 Seconds  
(without alignments)  
9156.102 Million cell updates/sec

Title: US-09-852-261-5  
Perfect score: 523  
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
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12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
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18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
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24: em\_ph:\*  
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28: em\_un:\*  
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 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
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 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	523	100.0	523	6	AX147746	AX147746 Sequence
2	523	100.0	523	6	AX300783	AX300783 Sequence
3	467.4	89.4	517	6	AX147742	AX147742 Sequence
4	467.4	89.4	517	6	AX300779	AX300779 Sequence
5	409	78.2	471	6	AX147754	AX147754 Sequence
6	409	78.2	471	6	AX300791	AX300791 Sequence
7	364.8	69.8	1536	10	BC012409	BC012409 Mus muscu
8	361.6	69.1	798	10	RNIGFI2	X06108 Rat mRNA (c
9	361.6	69.1	958	10	RNIGFI1	X06107 Rat mRNA (c
10	358.4	68.5	710	10	RATIGFIA	M15480 Rat insulin
11	356.8	68.2	539	6	AX147744	AX147744 Sequence
12	356.8	68.2	539	6	AX300781	AX300781 Sequence
13	349.4	66.8	651	10	MMIGFIBR	X04482 Mouse mRNA
14	336	64.2	432	4	AF022961	AF022961 Oryctolag
15	334.4	63.9	7260	6	AX375028	AX375028 Sequence
16	334.4	63.9	7260	6	AX411095	AX411095 Sequence
17	334.4	63.9	7260	9	HSIGFACI	X57025 Human IGF-I
18	332.8	63.6	666	6	A29119	A29119 H.sapiens I
19	332.8	63.6	725	9	HSIGFI	X00173 Homo sapien
20	332.8	63.6	728	9	HUMGFII	M29644 Human insul
21	332.4	63.6	616	9	HSIGF1A	X56773 H.sapiens m
22	331.2	63.3	620	6	I08370	I08370 Sequence 2
23	331.2	63.3	1076	9	HUMIGFI	M27544 Human insul
24	316.8	60.6	444	9	HSU40870	U40870 Human alter
25	293.8	56.2	532	4	SSIIGF1M	X17492 Porcine mRN
26	293.8	56.2	567	4	PIGGFIIA	M31175 Pig insulin
27	286.2	54.7	888	4	ECU85272	U85272 Equus cabal
28	281.8	53.9	978	4	GOTIGFI	D11378 Goat mRNA f
29	281.8	53.9	978	6	E05279	E05279 DNA encodin
30	280.2	53.6	1284	4	BTILGF1A	X15726 Bovine mRNA
31	275.4	52.7	747	4	SHPIGFIA6	M31735 Sheep insul
32	275.4	52.7	790	4	SHPIGFIA21	M31734 Sheep insul
33	275.4	52.7	1015	4	SHPIGFIA46	M31736 Sheep insul

34	275.4	52.7	1107	4	SHPIGFIA1	M30653 Sheep insul
35	275.2	52.6	730	9	HSIGF1B	X56774 H.sapiens m
36	275.2	52.6	1094	9	HUMGFIB	M11568 Human insul
37	275.2	52.6	1136	6	E01349	E01349 cDNA encodi
38	275.2	52.6	1136	6	I08009	I08009 Sequence 3
39	274.6	52.5	3599	6	BD063790	BD063790 Insulin-l
40	274.6	52.5	3599	6	BD069041	BD069041 Treatment
41	274.6	52.5	3600	6	BD063789	BD063789 Insulin-l
42	274.6	52.5	3600	6	BD069040	BD069040 Treatment
43	273.6	52.3	612	9	HUMIGFIB	M37484 Human insul
44	271.6	51.9	696	10	MMIGFIAR	X04480 Mouse mRNA
45	268.4	51.3	513	26	RNMGJIL	M17714 Rat insulin

## ALIGNMENTS

## RESULT 1

AX147746

LOCUS	AX147746	523 bp	DNA	linear	PAT 31-AUG-2001
-------	----------	--------	-----	--------	-----------------

DEFINITION Sequence 5 from Patent WO0136483.

ACCESSION AX147746

VERSION AX147746.1 GI:14346791

## KEYWORDS

SOURCE *Oryctolagus cuniculus* (rabbit)

ORGANISM *Oryctolagus cuniculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

## REFERENCE

AUTHORS Goldspink, G.R. and Johnson, I.R.

TITLE Use of the insulin-like-growth factor i isoform mgf for the treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 5 25-MAY-2001;

University College London (GB)

## FEATURES

Location/Qualifiers

source

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/db xref="taxon:9986"
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CDS

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/codon start=1
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/db_xref="REMTREMBL:CAC41177"
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DECCFRSCDLRRLEMYCAPLKPAKAARSVRAQRHTDMPKTQKYQPPSTNKKMKSQRRR

KGSTFEEHK"

BASE COUNT	154 a	129 c	142 g	98 t
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## ORIGIN

Query Match 100.0%; Score 523; DB 6; Length 523;

Best Local Similarity 100.0%; Pred. No. 9.5e-150;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

[illegible]

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Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120  
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Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

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Db 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360  
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Db 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420  
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Db 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420

Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480  
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Db 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy 481 CAAAGATGGCATTTCGCCCAATGAAATACACAAGTAAACATTC 523  
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Db 481 CAAAGATGGCATTTCGCCCAATGAAATACACAAGTAAACATTC 523

# RESULT 2

AX300783

LOCUS AX300783 523 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 5 from Patent WO0185781.

ACCESSION AX300783

VERSION AX300783.1 GI:17382064

KEYWORDS

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 5 15-NOV-2001;  
 University College London (GB) ; East Grinstead Medical Research  
 Trust (GB)

FEATURES

source Location/Qualifiers  
 1. .523  
 /organism="Oryctolagus cuniculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9986"



CDS

<1. .336  
/note="unnamed protein product"  
/codon\_start=1  
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/db\_xref="GI:17382065"  
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KGSTFEEHK"

BASE COUNT        154 a        129 c        142 g        98 t  
ORIGIN

Query Match                    100.0%;    Score 523;    DB 6;    Length 523;  
Best Local Similarity    100.0%;    Pred. No. 9.5e-150;  
Matches 523;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      |||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
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Db    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 3

AX147742

LOCUS            AX147742            517 bp        DNA        linear        PAT 31-AUG-2001  
DEFINITION    Sequence 1 from Patent W00136483.  
ACCESSION    AX147742



Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420  
 |||||  
 Db 358 CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416  
 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480  
 |||||  
 Db 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476  
 Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521  
 |||||  
 Db 477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517

#### RESULT 4

AX300779

LOCUS AX300779 517 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 1 from Patent WO0185781.

ACCESSION AX300779

VERSION AX300779.1 GI:17382060

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 1 15-NOV-2001;  
 University College London (GB) ; East Grinstead Medical Research  
 Trust (GB)

FEATURES Location/Qualifiers

source

1. 517

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

CDS

<1..333

/note="unnamed protein product"

/codon\_start=1

/protein\_id="CAD13040.1"

/db\_xref="GI:17382061"

/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIV  
 DECCFRSCDLRRLEMYCAPLKPASRSVRAQRHTDMPKTQKYQPPSTNKNTKSQRRK  
 GSTFEEHK"

BASE COUNT 150 a 130 c 139 g 98 t

ORIGIN

Query Match 89.4%; Score 467.4; DB 6; Length 517;

Best Local Similarity 96.2%; Pred. No. 1.3e-132;

Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60  
 |||||

Db 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120  
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Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180  
 |||||  
 Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180  
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 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240  
 |||||  
 Db 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240  
 |||||  
 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300  
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 Db 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297  
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 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360  
 |||||  
 Db 298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357  
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 Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420  
 |||||  
 Db 358 CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 416  
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 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 480  
 |||||  
 Db 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 476  
 |||||  
 Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521  
 |||||  
 Db 477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517  
 |||||

# RESULT 5

AX147754

LOCUS AX147754 471 bp DNA linear PAT 08-JUN-2001

DEFINITION Sequence 13 from Patent WO0136483.

ACCESSION AX147754

VERSION AX147754.1 GI:14348552

KEYWORDS

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.R. and Johnson, I.R.

TITLE Use of the insulin-like-growth factor i isoform mgf for the  
 treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 13 25-MAY-2001;  
 University College London (GB)

FEATURES Location/Qualifiers

source

1. .471

/organism="Oryctolagus cuniculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:9986"

CDS

<1. .318

/note="unnamed protein product"

/codon\_start=1

/protein\_id="CAC41264.1"

/db\_xref="GI:14348553"

/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSSRRAPQTGIV  
DECCFRSCDLRRLEMYCAPLKPAAARSVRAQRHTDMPKTQKEVHLKNTSRGSAGNKN  
YRM"

BASE COUNT        132 a     118 c     131 g     90 t  
ORIGIN

Query Match                78.2%;    Score 409;    DB 6;    Length 471;  
Best Local Similarity    90.1%;    Pred. No. 1.3e-114;  
Matches 471;    Conservative    0;    Mismatches    0;    Indels    52;    Gaps    1;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCAAGACTCAG----- 255

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        |||
Db    256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
        |||
Db    309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
        |||
Db    369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
        |||
Db    429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 471
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RESULT 6

AX300791

LOCUS            AX300791                            471 bp     DNA     linear     PAT 30-NOV-2001

DEFINITION      Sequence 13 from Patent WO0185781.

ACCESSION       AX300791

VERSION          AX300791.1    GI:17382072

KEYWORDS

SOURCE            Oryctolagus cuniculus (rabbit)

ORGANISM          Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 13 15-NOV-2001;  
University College London (GB) ; East Grinstead Medical Research  
Trust (GB)

FEATURES Location/Qualifiers

source 1. .471  
/organism="Oryctolagus cuniculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9986"

CDS <1. .318  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAD13045.1"  
/db\_xref="GI:17382073"  
/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIV  
DECCFRSCDLRRLEMYCAPLKPAAARSVRAQRHTDMPKQTQKEVHLKNTSRGSAGNKN  
YRM"

BASE COUNT 132 a 118 c 131 g 90 t

ORIGIN

Query Match 78.2%; Score 409; DB 6; Length 471;  
Best Local Similarity 90.1%; Pred. No. 1.3e-114;  
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240
Db	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	241	ATGCCCAAGACTCAG-----	255
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	256	-----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	308
Qy	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	309	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	368
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT	480

Db 369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

QY 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523

Db 429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 471

# RESULT 7

BC012409

LOCUS BC012409 1536 bp mRNA linear ROD 16-APR-2003

DEFINITION Mus musculus insulin-like growth factor 1, mRNA (cdna clone MGC:18617 IMAGE:4194295), complete cds.

ACCESSION BC012409

VERSION BC012409.1 GI:15214568

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1536)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cdna sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1536)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Jeffrey E. Green, M.D.

cdna Library Preparation: Life Technologies, Inc.

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

# Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 24 Row: k Column: 11

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754307.

FEATURES	Location/Qualifiers
source	1. .1536 /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db_xref="taxon:10090" /clone="MGC:18617 IMAGE:4194295" /tissue_type="Liver, normal. 5 month old male mouse." /clone_lib="NCI_CGAP_Li9" /lab_host="DH10B" /note="Vector: pCMV-SPORT6"
gene	1. .1536 /gene="Igfl" /db_xref="LocusID:16000" /db_xref="MGI:96432"
CDS	28. .429 /codon_start=1 /product="insulin-like growth factor 1" /protein_id="AAH12409.1" /db_xref="GI:15214569" /db_xref="LocusID:16000" /translation="MSSSHLFYLA LCLLTFTSSTTAGPETLCGAELVDALQFVCGPRG FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKAARSIRAQRHTD MPKTQKSPSLSTNKKTKLQRRRKGSTFEEHK"
BASE COUNT	485 a 324 c 303 g 424 t
ORIGIN	

Query Match 69.8%; Score 364.8; DB 10; Length 1536;  
Best Local Similarity 83.2%; Pred. No. 6.6e-101;  
Matches 441; Conservative 0; Mismatches 82; Indels 7; Gaps 2;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	94	GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG	153
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	154	AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTGGAGGGCACCTCAG	213
Qy	121	ACAGGCATCGTGGATGAGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	214	ACAGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	273
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240



[illegible]

## RESULT 8

RNIGFI2

LOCUS	RNIGFI2	798 bp	mRNA	linear	ROD 12-SEP-1993
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DEFINITION Rat mRNA (clone IGF1AB2) for insulin-like growth factor I.

ACCESSION X06108 M32339 Y00429

VERSION X06108.1 GI:56426

**KEYWORDS** insulin-like growth factor I.

SOURCE *Rattus norvegicus* (Norway rat)

ORGANISM *Rattus norvegicus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

## REFERENCE

1.

AUTHORS Shimatsu, A. and Rotwein, P.

TITLE Sequence of Two Rat Insulin-like Growth Factor I mRNAs Differing  
Within the 5' Untranslated Region

JOURNAL Nucleic Acids Res. 15 (1987) In press

## REFERENCE

2 (bases 1 to 798)

AUTHORS      Rotwein, P.

TITLE Direct Submission

JOURNAL Submitted (21-OCT-1987) Rotwein P., Washington University, School  
of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO  
63110, USA

COMMENT Another IGF-I mRNA of rat liver differing in the 5' UT-region is described in <X06107>.

FEATURE'S	Location/Qualifiers
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source      1.  .798
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/organism="Rattus norvegicus"
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/mol type="mRNA"
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/strain="Sprague-Dawley"
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/db xref="taxon:10116"
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/tissue type="liver"
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misc feature      1.  .72
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CDS
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    SATAGPETLCGAELVDALQFVCGPRGFYFNKPTGYGSSIRRAPQTGI VDECCFRSCDL
    RRLEMYCAPLKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
misc_feature
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    /note="3' UT-region"
BASE COUNT      238 a      196 c      183 g      181 t
ORIGIN

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Query Match          69.1%;  Score 361.6;  DB 10;  Length 798;
Best Local Similarity 82.8%;  Pred. No. 5.8e-100;
Matches 439;  Conservative 0;  Mismatches 84;  Indels 7;  Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db     217 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 276

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     277 AGGGGCTTTTACTTCAACAAGCCCAAGGCTATGGCTCCAGCATTCCGAGGGCACCACAG 336

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db     337 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 396

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db     397 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCAGCGCCACACTGAC 456

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     457 ATGCCCAAGACTCAGAAGTCCCAGCCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 516

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     517 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 576

Qy     361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      ||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     577 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 636

Qy     421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
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Db     637 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 696

Qy     475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 523
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     697 CCATTTCAAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATT 746

```



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Db      463 AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCACAG 522
Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Db      523 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 582
Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
Db      583 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 642
Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Db      643 ATGCCCAAGACTCAGAAGTCCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 702
Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Db      703 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 762
Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
Db      763 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 822
Qy      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
Db      823 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 882
Qy      475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
Db      883 CCATTTCAAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 932

```

# RESULT 10

## RATIGFIA

LOCUS RATIGFIA 710 bp mRNA linear ROD 27-APR-1993

DEFINITION Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.

ACCESSION M15480

VERSION M15480.1 GI:204749

KEYWORDS growth factor; insulin-like growth factor.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 710)

AUTHORS Roberts,C.T. Jr., Lasky,S.R., Lowe,W.L. Jr., Seaman,W.T. and  
LeRoith,D.

TITLE Molecular cloning of rat insulin-like growth factor I complementary  
deoxyribonucleic acids: differential messenger ribonucleic acid  
processing and regulation by growth hormone in extrahepatic tissues

JOURNAL Mol. Endocrinol. 1 (3), 243-248 (1987)

MEDLINE 88288198

PUBMED 3453891

COMMENT Original source text: Rat (Sprague-Dawley) adult liver cDNA to  
mRNA, clone pRIGF-1-42.

Draft entry and computer-readable copy of sequence in [Mol.  
Endocrinol. (1987) In press] kindly

[illegible]

Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420  
 ||| ||||| ||| ||||| ||| ||| ||| ||||| ||| |||||  
 Db 532 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 591

Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 592 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 651

Qy 475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 652 CCATTTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 701

# RESULT 11

AX147744

LOCUS AX147744 539 bp DNA linear PAT 31-AUG-2001

DEFINITION Sequence 3 from Patent WO0136483.

ACCESSION AX147744

VERSION AX147744.1 GI:14346789

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1

AUTHORS Goldspink, G.R. and Johnson, I.R.

TITLE Use of the insulin-like-growth factor i isoform mgf for the  
 treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 3 25-MAY-2001;  
 University College London (GB)

FEATURES Location/Qualifiers

source

1..539

/organism="Rattus norvegicus"

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/db\_xref="taxon:10116"

CDS

<1..336

/note="unnamed protein product"

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/db\_xref="GI:14346790"

/db\_xref="REMTREMBL:CAC41176"

/translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV  
 DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKSQPLSTHKRKLQRRR  
 KGSTLEEHK"

BASE COUNT 161 a 136 c 139 g 103 t

ORIGIN

Query Match 68.2%; Score 356.8; DB 6; Length 539;

Best Local Similarity 82.3%; Pred. No. 1.6e-98;

Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60

||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTTCGTGTGTGGACCA 60

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

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Db      61  AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTCCGAGGGCACCACAG 120
Qy      121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Db      121  ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qy      181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Qy      241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Db      241  ATGCCCAAGACTCAGAAGTCCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
Qy      301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Db      301  AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
Qy      361  CAGGATGTAGGAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
Db      361  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
Qy      421  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGTATC 474
Db      421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
Qy      475  ACATTTCAAAGAT-GGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
Db      481  TCATTTCAGAGATGGGCATTTCCTCAATGAAATACACAAGTAAACATTTC 530

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# RESULT 12

AX300781

LOCUS AX300781 539 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 3 from Patent WO0185781.

ACCESSION AX300781

VERSION AX300781.1 GI:17382062

KEYWORDS

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 3 15-NOV-2001;  
University College London (GB) ; East Grinstead Medical Research  
Trust (GB)

FEATURES Location/Qualifiers

source 1..539

/organism="Rattus sp."

/mol\_type="genomic DNA"

/db\_xref="taxon:10118"

CDS <1..336

/note="unnamed protein product"

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/db\_xref="GI:17382063"  
/translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV  
DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKSQPLSTHKRKLQRRR  
KGSTLEEHK"

BASE COUNT      161 a      136 c      139 g      103 t  
ORIGIN

Query Match            68.2%;    Score 356.8;    DB 6;    Length 539;  
Best Local Similarity    82.3%;    Pred. No. 1.6e-98;  
Matches 436;    Conservative    0;    Mismatches 87;    Indels    7;    Gaps    2;

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      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 AGGGGCTTTTACTTCAACAAGCCCAAGTCTATGGCTCCAGCATTTCGGAGGGCACCACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 CAGAATGTAGGAGGAGCCTCCCCAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
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Qy    475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
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Db    481 TCATTTCAGAGATGGGCAATTTCCCTCAATGAAATACACAAGTAAACATTTC 530
```

#### RESULT 13

MMIGFIBR

LOCUS            MMIGFIBR                            651 bp      mRNA      linear    ROD 21-MAR-1995

DEFINITION      Mouse mRNA for preproinsulin-like growth factor IB.

ACCESSION       X04482

VERSION          X04482.1    GI:51806

KEYWORDS        growth factor; insulin-like growth factor IB; preproinsulin-like



```

growth factor IB; signal peptide.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 651)
AUTHORS     Bell,G.I., Stempien,M.M., Fong,N.M. and Rall,L.B.
TITLE       Sequences of liver cDNAs encoding two different mouse insulin-like
            growth factor I precursors
JOURNAL      Nucleic Acids Res. 14 (20), 7873-7882 (1986)
MEDLINE     87040760
PUBMED      3774549

```

COMMENT The sequence is identical to the preproIGF-IA sequence (X04480) except for the presence of a 52 bp insertion following codon 86 (position 397 to 448), caused by alternative RNA splicing. The B domain of IGF comprises residues 1-29 (position 139-225), the C domain residues 30-41 (position 226-261), the A domain residues 42-62 (position 262-324) and the D domain residues 63-70 (position 325-348).

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FEATURES             Location/Qualifiers
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     CDS                73. .474
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                        /codon_start=1
                        /protein_id="CAA28170.1"
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                        /db_xref="SWISS-PROT:P05018"
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MPKTQKSPSLSTNKKTKLQRRRKGSTFEEHK"
     sig_peptide       73. .138
                        /note="signal peptide (aa -22 to -1)"
     mat_peptide       139. .348
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     misc_feature      349. .471
                        /note="COOH-terminal peptide (E domain) (aa 71 to 111)"
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BASE COUNT	193 a	185 c	149 g	124 t
ORIGIN				

Query Match 66.8%; Score 349.4; DB 10; Length 651;  
Best Local Similarity 82.8%; Pred. No. 3.2e-96;  
Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;

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Db 139 GGACCAGAGACCCCTTTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGACCG 198

Qy 61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120  
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 Db 199 AGGGGCTTTTACTTCAACAAGCCCAAGGCTATGGCTCCAGCATTTCGGAGGGCACCTCAG 258  
 Qy 121 ACAGGCATCGTGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180  
 |||||  
 Db 259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318  
 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240  
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 Db 319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCAGCGCCACACTGAC 378  
 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300  
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 Db 379 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438  
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360  
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 Db 439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498  
 Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420  
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 Db 499 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558  
 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474  
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 Db 559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618  
 Qy 475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506  
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 Db 619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651

# RESULT 14

AF022961

LOCUS AF022961 432 bp mRNA linear MAM 14-OCT-1997

DEFINITION Oryctolagus cuniculus insulin-like growth factor IB (IGF-IB) mRNA, complete cds.

ACCESSION AF022961

VERSION AF022961.1 GI:2522201

KEYWORDS

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 432)

AUTHORS Flekna,G., Brem,G. and Mueller,M.

TITLE Direct Submission

JOURNAL Submitted (05-SEP-1997) Institute of Animal Breeding and Genetics, Veterinary University of Vienna, Veterinaerplatz 1, Vienna A-1210, Austria

FEATURES Location/Qualifiers

source

1..432

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/strain="ZIKA hybrid strain"

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CDS       1. .432
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ALQFVCGDRGFYFNKPTGYGSSRRAPQTGIVDECCFRSCDLRRLMYCAPLKPAAK
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BASE COUNT      105 a      126 c      115 g      86 t
ORIGIN

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Query Match          64.2%;  Score 336;  DB 4;  Length 432;
Best Local Similarity 100.0%;  Pred. No. 4.1e-92;
Matches 336;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db      157 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 216
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Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db      217 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 276
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Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db      277 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 336
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Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      337 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 396
      |||
Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAG 336
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Db      397 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAG 432
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# RESULT 15

AX375028

```

LOCUS      AX375028          7260 bp :   DNA       linear   PAT 01-MAR-2002
DEFINITION Sequence 31 from Patent WO0210436.
ACCESSION  AX375028
VERSION    AX375028.1  GI:19169860
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1  
AUTHORS Baak,J. and Mutter,G.L.  
TITLE Prognostic classification of breast cancer  
JOURNAL Patent: WO 0210436-A 31 07-FEB-2002;  
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)

FEATURES Location/Qualifiers  
source 1. .7260  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 2330 a 1415 c 1240 g 2275 t  
ORIGIN

Query Match 63.9%; Score 334.4; DB 6; Length 7260;  
Best Local Similarity 84.6%; Pred. No. 2e-91;  
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Db    311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db    371 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db    551 ATGCCCAAGACCCAG----- 565

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGGATGTAGGAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
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Db    619 CAGGATGTAGGAAGACCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db    679 CTCTGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 523
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

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and is derived by analysis of the total score distribution.

# SUMMARIES

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1	523	100.0	523	22	AAD06400	Rabbit IGF-I isofo	
2	523	100.0	523	24	AAS16879	Rabbit mechano-gro	
3	523	100.0	553	18	AAT84893	Rabbit insulin lik	
4	467.4	89.4	517	22	AAD06398	Human IGF-I isofo	
5	467.4	89.4	517	24	AAS16877	Human mechano-grow	
6	409	78.2	471	22	AAD06405	Rabbit liver-type	
7	409	78.2	471	24	AAS16884	Rabbit insulin-lik	
8	356.8	68.2	539	22	AAD06399	Rat IGF-I isoform	
9	356.8	68.2	539	24	AAS16878	Rat mechano-growth	
10	349.4	66.8	651	25	ABV76185	Mouse insulin-like	
11	334.4	63.9	818	8	AAN70436	Sequence encoding	
12	334.4	63.9	7260	24	ABT11091	Human breast cance	
13	334.4	63.9	7260	24	ABK84583	Human cDNA differe	
14	334.4	63.9	7260	24	ABN97244	Gene #3742 used to	
15	334.4	63.9	7260	24	ABK64812	Human benign prost	
16	334.4	63.9	7260	24	ABK35504	Human endometrial	
17	334.4	63.9	7260	24	ABK35561	Gene IGF1 differen	
18	332.8	63.6	777	18	AAT84894	Human insulin like	
19	331.2	63.3	622	7	AAN60490	Human prepro-somat	
20	281.8	53.9	978	14	AAQ47804	Sequence encoding	
21	275.2	52.6	1136	8	AAN70435	Sequence encoding	
22	274.6	52.5	3599	19	AAV50428	Plasmid pIG0552 lo	
23	274.6	52.5	3599	19	AAV40796	Actual sequence of	
24	274.6	52.5	3600	19	AAV50427	Plasmid pIG0552 up	
25	274.6	52.5	3600	19	AAV40795	Expected sequence	
26	274.6	52.5	5707	20	AAX88055	Plasmid pIG0335 DN	
27	274.6	52.5	6345	20	AAX88054	Plasmid pIG0100A D	
28	273.6	52.3	612	22	AAS14695	Human cDNA encodin	
29	273.6	52.3	612	25	ABZ83309	Toxicologically re	
30	266.8	51.0	1052	20	AAX27498	Rat liver form of	
31	262	50.1	487	22	AAD06404	Rat liver-type IGF	
32	262	50.1	487	24	AAS16883	Rat insulin-like g	
33	250	47.8	671	24	ABT09479	Phase-1 Rat CT gen	
34	237.6	45.4	317	24	AAS16882	Human insulin-like	
35	237.6	45.4	318	22	AAD06403	Human liver-type I	
36	237.6	45.4	462	19	AAV50426	Human IGF-1 encodi	
37	237.6	45.4	462	19	AAV40794	Human IGF-I coding	
38	237.6	45.4	462	24	ABZ35734	Human IGF1 polynuc	
39	237.6	45.4	462	24	ABX09977	Human IGF1 DNA fra	
40	237.6	45.4	462	24	ABV78158	Human IGF1 DNA SEQ	
41	237.6	45.4	462	24	ABL91699	Human polynucleoti	
42	209	40.0	286	25	ABV76186	Mouse insulin-like	
43	193	36.9	210	24	AAD45568	Human insulin-like	
44	193	36.9	210	24	AAD44955	Human insulin grow	
45	193	36.9	210	24	ABA03146	Native mature IGF-	

# ALIGNMENTS

RESULT 1

AAD06400

ID AAD06400 standard; cDNA; 523 BP.

XX

AC AAD06400;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;  
 KW mechano-growth factor; neurological disorder; neurodegenerative disorder;  
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;  
 KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;  
 KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;  
 KW sex-linked muscular dystrophy; peripheral neuropathy;  
 KW Alzheimer's disease; Parkinson's disease; ss.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /\*tag= a

FT /product= "Mechano-growth factor (MGF)"

FT /note= "This region comprises exons 3-6. The CDS does  
 FT not include start codon"

FT /partial

XX

PN WO200136483-A1.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-GB04354.

XX

PR 15-NOV-1999; 99GB-0026968.

XX

PA (UNLO ) UNIV COLLEGE LONDON.

XX

PI Goldspink G, Johnson I;

XX

DR WPI; 2001-355620/37.

DR P-PSDB; AAE02449.

XX

PT Use of mechano-growth factor, an isoform of Insulin-like Growth  
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a  
 PT medicament for the treatment of neurological disorder -

XX

PS Claim 4; Page 53-54; 66pp; English.

XX

CC The present invention relates to use of mechano-growth factor (MGF),  
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a  
 CC medicament for the treatment of neurological disorder. The MGF is capable  
 CC of reducing motoneurone loss by 20% or greater in response to nerve  
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone  
 CC rescue. The MGF polynucleotide and polypeptide are useful in the  
 CC manufacture of a medicament for the treatment of a neurological disorder,  
 CC including a disorder of motoneurons and/or neurodegenerative disorder,

CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive  
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,  
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a  
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an  
 CC injury that affects motoneurons, motoneurone loss associated with aging,  
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,  
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.  
 CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle  
 CC isoform having extracellular (Ec) domain, hence also referred as  
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by  
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame  
 CC of MGF.

XX

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 100.0%; Score 523; DB 22; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-144;  
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      |||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA 360
      |||
Db    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA 360

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420
      |||
Db    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
      |||
Db    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523

```

RESULT 2



AAS16879

ID AAS16879 standard; cDNA; 523 BP.

XX

AC AAS16879;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rabbit mechano-growth factor (MGF) cDNA.

XX

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;  
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;  
KW muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;  
KW nerve avulsion.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /\*tag= a

FT /product= "Rabbit MGF"

FT /partial

FT /note= "No start codon"

FT exon 1..76

FT /\*tag= b

FT /number= 3

FT exon 77..259

FT /\*tag= c

FT /number= 4

FT exon 260..309

FT /\*tag= d

FT /number= 5

FT exon 311..333

FT /\*tag= e

FT /number= 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO ) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10561.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as

PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has

PT ability to reduce motoneuron loss in response to nerve avulsion, to

PT treat nerve damage -

XX

PS Disclosure; Fig 7; 65pp; English.

XX

CC The invention relates to the use of an insulin-like growth factor I  
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture  
CC of a medicament for treating nerve damage in the peripheral nervous  
CC system, or for treating nerve damage by localising MGF at the site of  
CC damage. The nerve damage may include severing of a nerve. The treatment  
CC may be combined with another treatment (such as a polypeptide growth  
CC factor other than MGF) that prevents or diminishes degeneration of the  
CC target organ (for example, muscle) which the damaged nerve innervates,  
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding  
CC MGF prevents or diminishes degeneration. The method is useful for  
CC treating neurological disorders, preferably motoneuron disorders. These  
CC methods can reduce motoneuron loss by 20% or greater in response to nerve  
CC avulsion. This sequence represents cDNA encoding the rabbit MGF.

XX

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 100.0%; Score 523; DB 24; Length 523;  
Best Local Similarity 100.0%; Pred. No. 5.1e-144;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60  
|||  
Db 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60  
  
Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120  
|||  
Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120  
  
Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180  
|||  
Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180  
  
Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240  
|||  
Db 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240  
  
Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300  
|||  
Db 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300  
  
Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360  
|||  
Db 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360  
  
Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420  
|||  
Db 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420  
  
Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480  
|||  
Db 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480  
  
Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523  
|||  
Db 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523

RESULT 3

AAT84893

ID AAT84893 standard; cDNA; 553 BP.

XX

AC AAT84893;

XX

DT 14-APR-1998 (first entry)

XX

DE Rabbit insulin like growth factor 1 encoding cDNA.

XX

KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;  
KW heart; neuromuscular disease; primer; ss.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..366

FT /\*tag= a

FT /product= "IGF-1"

XX

PN WO9733997-A1.

XX

PD 18-SEP-1997.

XX

PF 11-MAR-1997; 97WO-GB00658.

XX

PR 11-MAR-1996; 96GB-0005124.

XX

PA (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.

XX

PI Goldspink G;

XX

DR WPI; 1997-470877/43.

DR P-PSDB; AAW23301.

XX

PT Use of insulin like growth factor I characterised by presence of Ec  
PT peptide - to treat humans or animals, particularly muscle disorders,  
PT heart conditions or neuromuscular diseases

XX

PS Disclosure; Fig 3; 33pp; English.

XX

CC A use of insulin like growth factor I (IGF-1) has been developed, and  
CC is characterised by the presence of the Ec peptide, or a functional  
CC equivalent, in the treatment or therapy of a human or animal. The IGF-1  
CC polypeptide can be used to treat muscular disorders, e.g. Duchenne or  
CC Becker muscular dystrophy, autosomal dystrophies and related progressive  
CC skeletal muscle weakness and wasting, muscle atrophy in ageing humans,  
CC spinal cord injury induced muscle atrophy and neuromuscular diseases,  
CC and cardiac disorders, e.g. diseases where promotion of cardiac muscle  
CC protein synthesis is a beneficial treatment, cardiomyopathies and acute  
CC heart failure or insult, specifically myocarditis or myocardial  
CC infarction. It can also be used to promote bone fracture healing and  
CC maintenance of bone in old age. The present sequence encodes rabbit  
CC IGF-1 used in the present specification.

XX

SQ Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;

Query Match 100.0%; Score 523; DB 18; Length 553;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-144;  
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      91 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db     151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db     211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 270

Qy     241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db     271 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db     331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy     361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db     391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy     421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db     451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy     481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
      |||
Db     511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553
  
```

#### RESULT 4

AAD06398

ID AAD06398 standard; cDNA; 517 BP.

XX

AC AAD06398;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

KW sex-linked muscular dystrophy; peripheral neuropathy;  
 KW Alzheimer's disease; Parkinson's disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..333  
 FT /\*tag= a  
 FT /product= "Mechano-growth factor (MGF)"  
 FT /note= "This region comprises exons 3-6. The CDS does  
 FT not include start codon"  
 FT /partial  
 XX  
 PN WO200136483-A1.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 15-NOV-2000; 2000WO-GB04354.  
 XX  
 PR 15-NOV-1999; 99GB-0026968.  
 XX  
 PA (UNLO ) UNIV COLLEGE LONDON.  
 XX  
 PI Goldspink G, Johnson I;  
 XX  
 DR WPI; 2001-355620/37.  
 DR P-PSDB; AAE02447.  
 XX  
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth  
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a  
 PT medicament for the treatment of neurological disorder -  
 XX  
 PS Claim 4; Page 49-50; 66pp; English.  
 XX  
 CC The present invention relates to use of mechano-growth factor (MGF),  
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a  
 CC medicament for the treatment of neurological disorder. The MGF is capable  
 CC of reducing motoneurone loss by 20% or greater in response to nerve  
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone  
 CC rescue. The MGF polynucleotide and polypeptide are useful in the  
 CC manufacture of a medicament for the treatment of a neurological disorder,  
 CC including a disorder of motoneurons and/or neurodegenerative disorder,  
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive  
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,  
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a  
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an  
 CC injury that affects motoneurons, motoneurone loss associated with aging,  
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,  
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.  
 CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle  
 CC isoform having extracellular (Ec) domain, hence also referred as  
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by  
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame  
 CC of MGF.  
 XX  
 SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 89.4%; Score 467.4; DB 22; Length 517;  
 Best Local Similarity 96.2%; Pred. No. 1.3e-127;  
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||
Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        |||
Db    241 ATGCCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        |||
Db    298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
        |||
Db    358 CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
        |||
Db    417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521
        |||
Db    477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
  
```

# RESULT 5

AAS16877

ID AAS16877 standard; cDNA; 517 BP.

XX

AC AAS16877;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human mechano-growth factor (MGF) cDNA.

XX

KW Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;  
 KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;  
 KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;  
 KW nerve avulsion.

XX

OS Homo sapiens..

XX

Key	Location/Qualifiers
FT CDS	1..333
FT	/*tag= a
FT	/product= "Human MGF"
FT	/partial
FT	/note= "No start codon"
FT exon	1..76
FT	/*tag= b
FT	/number= 3
FT exon	77..259
FT	/*tag= c
FT	/number= 4
FT exon	260..307
FT	/*tag= d
FT	/number= 5
FT exon	308..330
FT	/*tag= e
FT	/number= 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO ) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10559.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as

PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has

PT ability to reduce motoneuron loss in response to nerve avulsion, to

PT treat nerve damage -

XX

PS Claim 11; Fig 5; 65pp; English.

XX

CC The invention relates to the use of an insulin-like growth factor I

CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture

CC of a medicament for treating nerve damage in the peripheral nervous

CC system, or for treating nerve damage by localising MGF at the site of

CC damage. The nerve damage may include severing of a nerve. The treatment

CC may be combined with another treatment (such as a polypeptide growth

CC factor other than MGF) that prevents or diminishes degeneration of the

CC target organ (for example, muscle) which the damaged nerve innervates,

CC whereby the treatment of the muscle with MGF or a polynucleotide encoding

CC MGF prevents or diminishes degeneration. The method is useful for

CC treating neurological disorders, preferably motorneuron disorders. These

CC methods can reduce motoneuron loss by 20% or greater in response to nerve

CC avulsion. This sequence represents cDNA encoding the human MGF.

XX

SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 89.4%; Score 467.4; DB 24; Length 517;  
Best Local Similarity 96.2%; Pred. No. 1.3e-127;  
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db    181 TGTGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db    358 CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521
      |||
Db    477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
```

RESULT 6

AAD06405

ID AAD06405 standard; cDNA; 471 BP.

XX

AC AAD06405;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.

XX

KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;



KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;  
 KW sex-linked muscular dystrophy; peripheral neuropathy;  
 KW Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.  
 XX  
 OS *Oryctolagus cuniculus*.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..318  
 FT /\*tag= a  
 FT /product= "Liver-type IGF-I isoform (L.IGF-I)"  
 FT /transl\_except= (pos:7..9, aa:Gln)  
 FT /transl\_except= (pos:25..27, aa:Gln)  
 FT /note= "These translation exceptions occur while decoding  
 FT the alternative version of the protein (AAE02456).  
 FT The CDS comprises exons 3, 4 and 6 and  
 FT does not include start codon"  
 FT /partial  
 XX  
 PN WO200136483-A1.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 15-NOV-2000; 2000WO-GB04354.  
 XX  
 PR 15-NOV-1999; 99GB-0026968.  
 XX  
 PA (UNLO ) UNIV COLLEGE LONDON.  
 XX  
 PI Goldspink G, Johnson I;  
 XX  
 DR WPI; 2001-355620/37.  
 DR P-PSDB; AAE02452, AAE02456.  
 XX  
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth  
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a  
 PT medicament for the treatment of neurological disorder -  
 XX  
 PS Disclosure; Page 59-60; 66pp; English.  
 XX  
 CC The present invention relates to use of mechano-growth factor (MGF),  
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a  
 CC medicament for the treatment of neurological disorder. The MGF is capable  
 CC of reducing motoneurone loss by 20% or greater in response to nerve  
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone  
 CC rescue. The MGF polynucleotide and polypeptide are useful in the  
 CC manufacture of a medicament for the treatment of a neurological disorder,  
 CC including a disorder of motoneurons and/or neurodegenerative disorder,  
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive  
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,  
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a  
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an  
 CC injury that affects motoneurons, motoneurone loss associated with aging,  
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,  
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.  
 CC The present sequence is rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.  
 CC The L.IGF-I protein comprises amino acid sequences encoded by  
 CC nucleic acid sequence of IGF-I exons 4 and 6.

XX

SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match 78.2%; Score 409; DB 22; Length 471;  
Best Local Similarity 90.1%; Pred. No. 2e-110;  
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    241 ATGCCCAAGACTCAG----- 255

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db    256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db    309 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 368

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
      |||
Db    429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 471
```

RESULT 7

AAS16884

ID AAS16884 standard; cDNA; 471 BP.

XX

AC AAS16884;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rabbit insulin-like growth factor I liver-type isoform (L.IGF-I) cDNA.

XX

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;

KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;

KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;

KW nerve avulsion; insulin-like growth factor I liver-type isoform; L.IGF-I;  
XX  
OS *Oryctolagus cuniculus*.

XX  
FH Key Location/Qualifiers  
FT CDS 1..318  
FT /\*tag= a  
FT /product= "Rabbit L.IGF-I"  
FT /partial  
FT /note= "No start codon"  
FT exon 1..75  
FT /\*tag= b  
FT /number= exon 3  
FT exon 76..258  
FT /\*tag= c  
FT /number= exon 4  
FT exon 259..315  
FT /\*tag= d  
FT /number= exon 6

XX  
PN WO200185781-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 10-MAY-2001; 2001WO-GB02054.  
XX  
PR 10-MAY-2000; 2000GB-0011278.  
XX  
PA (UNLO ) UNIV COLLEGE LONDON.  
PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX  
PI Goldspink G, Terenghi G;

XX  
DR WPI; 2002-055585/07.  
DR P-PSDB; AAU10564.

XX  
PT Use of insulin-like growth factor I (IGF-I) isoform known as  
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has  
PT ability to reduce motoneuron loss in response to nerve avulsion, to  
PT treat nerve damage -

XX  
PS Disclosure; Fig 10; 65pp; English.

XX  
CC The invention relates to the use of an insulin-like growth factor I  
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture  
CC of a medicament for treating nerve damage in the peripheral nervous  
CC system, or for treating nerve damage by localising MGF at the site of  
CC damage. The nerve damage may include severing of a nerve. The treatment  
CC may be combined with another treatment (such as a polypeptide growth  
CC factor other than MGF) that prevents or diminishes degeneration of the  
CC target organ (for example, muscle) which the damaged nerve innervates,  
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding  
CC MGF prevents or diminishes degeneration. The method is useful for  
CC treating neurological disorders, preferably motoneuron disorders. These  
CC methods can reduce motoneuron loss by 20% or greater in response to nerve  
CC avulsion. This sequence represents cDNA encoding the rabbit insulin-like  
CC growth factor I liver-type isoform (L.IGF-I) used in experiments on

CC motoneuron loss.

XX

SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match 78.2%; Score 409; DB 24; Length 471;  
Best Local Similarity 90.1%; Pred. No. 2e-110;  
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    241 ATGCCCCAAGACTCAG----- 255

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db    256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db    309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 480
      |||
Db    369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 428

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db    429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 471
```

RESULT 8

AAD06399

ID AAD06399 standard; cDNA; 539 BP.

XX

AC AAD06399;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rat IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;  
KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;  
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;  
KW sex-linked muscular dystrophy; peripheral neuropathy;  
KW Alzheimer's disease; Parkinson's disease; ss.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /\*tag= a

FT /product= "Mechano-growth factor (MGF)"

FT /note= "This region comprises exons 3-6. The CDS does

FT not include start codon"

FT /partial

XX

PN WO200136483-A1.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-GB04354.

XX

PR 15-NOV-1999; 99GB-0026968.

XX

PA (UNLO ) UNIV COLLEGE LONDON.

XX

PI Goldspink G, Johnson I;

XX

DR WPI; 2001-355620/37.

DR P-PSDB; AAE02448.

XX

PT Use of mechano-growth factor, an isoform of Insulin-like Growth  
PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a  
PT medicament for the treatment of neurological disorder -

XX

PS Claim 4; Page 51-52; 66pp; English.

XX

CC The present invention relates to use of mechano-growth factor (MGF),  
CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a  
CC medicament for the treatment of neurological disorder. The MGF is capable  
CC of reducing motoneurone loss by 20% or greater in response to nerve  
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone  
CC rescue. The MGF polynucleotide and polypeptide are useful in the  
CC manufacture of a medicament for the treatment of a neurological disorder,  
CC including a disorder of motoneurons and/or neurodegenerative disorder,  
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive  
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,  
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a  
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an  
CC injury that affects motoneurons, motoneurone loss associated with aging,  
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,  
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.  
CC The present sequence is rat IGF-I isoform MGF cDNA. MGF is a muscle  
CC isoform having extracellular (Ec) domain, hence also referred as  
CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by  
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame  
CC of MGF.

XX

SQ Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

Query Match 68.2%; Score 356.8; DB 22; Length 539;  
Best Local Similarity 82.3%; Pred. No. 5.1e-95;  
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 AGGGGCTTTTACTTCAACAAGCCCAAGTCTATGGCTCCAGCATTCCGAGGGGCACCACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCAGCGCCACACTGAC 240

Qy    241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 ATGCCCCAAGACTCAGAAGTCCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGTATC 474
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 530
```

RESULT 9

AAS16878

ID AAS16878 standard; cDNA; 539 BP.

XX

AC AAS16878;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rat mechano-growth factor (MGF) cDNA.

XX

KW Rat; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;

KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;

KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;

KW nerve avulsion.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /\*tag= a

FT /product= "Rat MGF"

FT /partial

FT /note= "No start codon"

FT exon 1..75

FT /\*tag= b

FT /number= exon 3

FT exon 76..258

FT /\*tag= c

FT /number= exon 4

FT exon 259..309

FT /\*tag= d

FT /number= exon 5

FT exon 310..333

FT /\*tag= e

FT /number= exon 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO ) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10560.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as

PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has

PT ability to reduce motoneuron loss in response to nerve avulsion, to

PT treat nerve damage -

XX

PS Disclosure; Fig 6; 65pp; English.

XX

CC The invention relates to the use of an insulin-like growth factor I

CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture

CC of a medicament for treating nerve damage in the peripheral nervous

CC system, or for treating nerve damage by localising MGF at the site of

CC damage. The nerve damage may include severing of a nerve. The treatment

CC may be combined with another treatment (such as a polypeptide growth

CC factor other than MGF) that prevents or diminishes degeneration of the

CC target organ (for example, muscle) which the damaged nerve innervates,

CC whereby the treatment of the muscle with MGF or a polynucleotide encoding

CC MGF prevents or diminishes degeneration. The method is useful for

CC treating neurological disorders, preferably motorneuron disorders. These

CC methods can reduce motoneuron loss by 20% or greater in response to nerve  
CC avulsion. This sequence represents cDNA encoding the rat MGF.  
XX  
SQ Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

Query Match 68.2%; Score 356.8; DB 24; Length 539;  
Best Local Similarity 82.3%; Pred. No. 5.1e-95;  
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTCCGGAGGGCACCACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 ACGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
        ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    481 TCATTTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 530
```

RESULT 10

ABV76185

ID ABV76185 standard; cDNA; 651 BP.

XX

AC ABV76185;

XX

DT 07-MAR-2003 (first entry)

XX

DE Mouse insulin-like growth factor IB cDNA.

XX

KW Insulin-like growth factor IB; IGF-IB; mouse; mRNA; assay;



KW nucleic acid detection; gene; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 73..474  
 FT /\*tag= a  
 FT /product= "IGF-IB"  
 XX  
 PN WO200297390-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 31-MAY-2002; 2002WO-SE01056.  
 XX  
 PR 01-JUN-2001; 2001SE-0001934.  
 XX  
 PA (BIOV-) BIOVITRUM AB.  
 XX  
 PI Parrow V, Rosengren L;  
 XX  
 DR WPI; 2003-129529/12.  
 XX  
 PT Quantitating a target nucleic acid in a sample comprises immobilizing,  
 PT on a solid support, a sample comprising a target nucleic acid, and  
 PT detecting and quantitating signals generated from the antisense and  
 PT sense probes -  
 XX  
 PS Example 1; Page 16-17; 18pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding murine insulin-like  
 CC growth factor 1B (IGF-IB). The cDNA was used in an example of the  
 CC method of the invention to generate probes for determination of  
 CC IGF-IB RNA. The method comprises a quantitative hybridisation  
 CC assay for analysis of mRNA in a target nucleic acid (TNA) sample.  
 CC It involves: (i) immobilising the TNA sample on a solid support;  
 CC (ii) contacting a labelled antisense probe to a first portion of the  
 CC TNA, and a labelled sense probe to a second portion of the TNA;  
 CC (iii) detecting and quantitating the signals generated from the  
 CC hybridised probes; and (iv) determining the value represented by  
 CC the antisense probe signal minus the sense probe signal, the value  
 CC being proportional to the amount of mRNA in the TNA sample. In an  
 CC example of the method, a cDNA clone containing 60 nucleotides from  
 CC exon 2 and 179 nucleotides from exon 3 of the mouse IGF-IB gene was  
 CC cloned into pGEN-4Z vector. Linearisation of the plasmid with  
 CC EcoRI allowed transcription of a 250-nucleotide antisense probe  
 CC using T7 polymerase. Linearisation with HindIII allowed  
 CC transcription of a sense probe of similar length using SP6  
 CC polymerase (see ABV76186). The probes were purified and used to  
 CC determine IGF-I RNA in mouse hepatocytes and also in rat hepatocytes.  
 XX  
 SQ Sequence 651 BP; 193 A; 185 C; 149 G; 124 T; 0 other;

Query Match 66.8%; Score 349.4; DB 25; Length 651;  
 Best Local Similarity 82.8%; Pred. No. 8.3e-93;  
 Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;



XX  
 PR 20-NOV-1986; 86US-0929671.  
 PR 07-JAN-1986; 86US-0816662.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Krivi GG, Rotwein PS;  
 XX  
 DR WPI; 1987-200203/29.  
 XX  
 PT New pre-pro-insulin-like growth factor-1 protein - obtd. by  
 PT recombinant DNA procedures for use as growth promoters for  
 PT enhancing lactation, for stimulating cell proliferation etc.  
 XX  
 PS Example; Fig 5; 59pp; English.  
 XX  
 CC A 42 base oligonucleotide corresponding to the DNA sequence encoding  
 CC amino acids 10 to 23 of mature human IGF-I was synthesized (AAN70437).  
 CC The radiolabeled 42 mer was then employed to screen for IGF-I  
 CC containing DNA sequences in a human liver cDNA library. Insulin-  
 CC like growth factors-1A and -1B cDNAs were isolated from a human cDNA  
 CC library by using lambdagt 11 (AAN70435, AAN70436). The human IGF-1  
 CC genomic gene was isolated and mapped. It encodes at least two  
 CC preproinsulin-like growth factor-1 proteins. An essentially pure  
 CC preproinsulin-like growth factor-1 protein comprising the sequence  
 CC of amino acids shown in Figure six is claimed (AAP70277).  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;

Query Match 63.9%; Score 334.4; DB 8; Length 818;  
 Best Local Similarity 84.6%; Pred. No. 2.4e-88;  
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      203 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 262

Qy      61 AGGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      263 AGGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 322

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      323 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 382

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      383 /TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 442

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      443 ATGCCCAAGACCCAG----- 457

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      458 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 510

```



CC The methods are also useful as a screening tool for agents that modulate  
CC the onset or progression of breast cancer. The breast cancer genes may be  
CC used as diagnostic markers for the prediction or identification of the  
CC malignant state of breast tissue, for confirming the type and progression  
CC of cancer, and for drug screening and assays. The present sequence is a  
CC coding sequence of the invention.

CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub.published\_pct\_sequences.

XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;  
Best Local Similarity 84.6%; Pred. No. 5.7e-88;  
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      371 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db     566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db     619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db     679 CTCTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 523
      |||
Db     739 TTAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATT 784
```

RESULT 13

ABK84583

ID ABK84583 standard; cDNA; 7260 BP.

XX

AC ABK84583;  
 XX  
 DT 14-AUG-2002 (first entry)  
 XX  
 DE Human cDNA differentially expressed in granulocytic cells #1154.  
 XX  
 KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KW viral infection; parasitic infection; protozoal infection;  
 KW fungal infection; sterile inflammatory disease; psoriasis;  
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KW adult respiratory distress syndrome; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; periodontal disease;  
 KW granulocyte activation; chronic inflammation; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200228999-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 03-OCT-2001; 2001WO-US30821.  
 XX  
 PR 03-OCT-2000; 2000US-237189P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
 XX  
 DR WPI; 2002-435328/46.  
 XX  
 PT Detecting granulocyte activation by detecting differential expression  
 PT of genes associated with granulocyte activation, which serves as  
 PT diagnostic markers that is useful for monitoring disease states and  
 PT drug toxicity -  
 XX  
 PS Claim 1; SEQ ID No 1154; 114pp; English.  
 XX  
 CC The invention relates to detecting (M1) granulocyte (GC) activation  
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 CC DNA chip analysis as given in the specification, and comparing  
 CC the expression level to an expression level in an unactivated  
 CC GC, where differential expression of Gs is indicative of GCA.  
 CC Also included are modulating (M2) GA by contacting GC with an agent  
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
 CC for an agent capable of modulating GCA or an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease using the  
 CC gene expression profile; (3) detecting (M4) an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease, by detecting the  
 CC level of expression in a sample of the tissue of gene(s) from Gs, where  
 CC the level of expression of the gene is indicative of inflammation;  
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
 CC an allergic response in a subject, exposure of a subject to a pathogen  
 CC or sterile inflammatory disease, by contacting a tissue having  
 CC inflammation with an agent that modulates the expression of gene(s)



Db

739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784

RESULT 14

ABN97244

ID ABN97244 standard; DNA; 7260 BP.

XX

AC ABN97244;

XX

DT 13-AUG-2002 (first entry)

XX

DE Gene #3742 used to diagnose liver cancer.

XX

KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;  
KW metastatic liver tumour; cytostatic; expression profile; disease state;  
KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX

OS Homo sapiens.

XX

PN WO200229103-A2.

XX

PD 11-APR-2002.

XX

PF 02-OCT-2001; 2001WO-US30589.

XX

PR 02-OCT-2000; 2000US-237054P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX

DR WPI; 2002-426119/45.

XX

PT Diagnosing and detecting the progression of liver cancer,  
PT hepatocellular carcinoma or metastatic liver tumor in a patient,  
PT involves detecting the level of expression of two or more genes in a  
PT liver tissue sample -

XX

PS Claim 1; SEQ ID NO 3742; 298pp; English.

XX

CC The invention relates to a novel method for diagnosing and detecting the  
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver  
CC tumour in a patient, and differentiating metastatic liver cancer from  
CC hepatocellular carcinoma in a patient, involving detecting the level of  
CC expression of two or more genes represented in ABN93503-ABN97455 in a  
CC tissue sample. The method of the invention has hepatotropic, and  
CC cytostatic activity. The method is useful for diagnosing and detecting  
CC the progression of liver cancer, hepatocellular carcinoma and metastatic  
CC liver carcinoma in a patient. The method is useful for identifying  
CC expression profiles which serve as useful diagnostic markers as well as  
CC markers that can be used to monitor disease states, disease progression,  
CC drug toxicity, drug efficacy and drug metabolism.

CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX



SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;  
Best Local Similarity 84.6%; Pred. No. 5.7e-88;  
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db     491 TGTGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db     566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db     619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db     679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db     739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784
```

RESULT 15

ABK64812

ID ABK64812 standard; DNA; 7260 BP.

XX

AC ABK64812;

XX

DT 18-JUN-2002 (first entry)

XX

DE Human benign prostatic hyperplasia gene #707.

XX

KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200212440-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 07-AUG-2001; 2001WO-US24708.  
 XX  
 PR 07-AUG-2000; 2000US-223323P.  
 PR 05-JUN-2001; 2001US-0873319.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 PA (NISB ) JAPAN TOBACCO INC.  
 XX  
 PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;  
 XX  
 DR WPI; 2002-257476/30.  
 XX  
 PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by  
 PT detecting expression levels of one or more genes in prostate cells from  
 PT patient that are differentially regulated compared to normal prostate  
 PT cells -  
 XX  
 PS Disclosure; Page 391-393; 444pp; English.  
 XX  
 CC The invention relates to a method of diagnosing (I) the onset or  
 CC progression of benign prostatic hyperplasia (BPH), or screening (II) for  
 CC or identifying an agent that modulates the onset or progression of BPH.  
 CC The method is based on changes in gene expression in BPH tissue isolated  
 CC from patients exhibiting different clinical states of prostate  
 CC hyperplasia as compared to normal prostate tissue. (I) comprises  
 CC detecting the expression levels of one or more genes in prostate cells  
 CC from the subject that are differentially regulated compared to normal  
 CC prostate cells. (II) comprises preparing a first gene expression profile  
 CC of BPH cells or BPH-like cell population, exposing the cells to the  
 CC agent, preparing a second gene expression profile of the agent exposed  
 CC cells, and comparing the first and second gene expression profiles.  
 CC (I) is useful for diagnosing the onset or progression of BPH. (II) is  
 CC useful for identifying an agent that modulates the onset or progression  
 CC of BPH. The methods are useful to present information identifying  
 CC the expression level in a tissue or cells, by comparing the expression  
 CC level of genes given in the specification in the tissue or cells to the  
 CC level of expression of gene in the database, and displaying the  
 CC expression levels of at least one gene in the tissue or cell sample  
 CC compared to the expression level in BPH. Agents using (II) are useful for  
 CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human  
 CC benign prostatic hyperplasia gene sequences of the invention.  
 XX  
 SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;  
 Best Local Similarity 84.6%; Pred. No. 5.7e-88;  
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60  
 |||||||||||||||||||  
 Db 311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 370  
 Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Db	371		AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	430
Qy	121		ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	431		ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181		TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240
Db	491		TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	550
Qy	241		ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	551		ATGCCCAAGACCCAG-----	565
Qy	301		AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	566		-----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA	618
Qy	361		CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG	420
Db	619		CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG	678
Qy	421		CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT	478
Db	679		CTCTGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT	738
Qy	479		TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC	523
Db	739		TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC	784

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Job time : 211.995 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 06:03:55 ; Search time 48.3585 Seconds  
(without alignments)  
4773.589 Million cell updates/sec

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Perfect score: 523  
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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	523	100.0	553	3	US-09-142-583A-3
2	523	100.0	553	3	US-09-142-583A-5
3	332.8	63.6	777	3	US-09-142-583A-10
4	331.2	63.3	622	6	5405942-2
5	274.6	52.5	5707	2	US-08-472-809B-8
6	274.6	52.5	6345	2	US-08-472-809B-7
7	234.4	44.8	357	6	5405942-13
8	232.8	44.5	357	6	5405942-9
9	191.4	36.6	210	6	5405942-7
10	191.4	36.6	210	6	5405942-11
11	191.4	36.6	2862	4	US-09-255-829-13

12	189.8	36.3	210	6	5405942-15	Patent No. 5405942
13	185.2	35.4	240	1	US-08-308-196A-1	Sequence 1, Appli
14	185.2	35.4	240	5	PCT-US91-06452-1	Sequence 1, Appli
15	185.2	35.4	390	3	US-09-029-267-13	Sequence 13, Appl
16	158.8	30.4	798	1	US-07-953-230A-6	Sequence 6, Appli
17	154.8	29.6	770	1	US-07-953-230A-1	Sequence 1, Appli
18	154.8	29.6	846	1	US-07-953-230A-5	Sequence 5, Appli
19	127	24.3	621	3	US-08-989-251-40	Sequence 40, Appl
20	127	24.3	621	3	US-09-340-250-40	Sequence 40, Appl
21	127	24.3	621	4	US-09-528-108-40	Sequence 40, Appl
22	125.8	24.1	233	1	US-08-444-142-3	Sequence 3, Appli
23	125.8	24.1	233	1	US-08-444-131-3	Sequence 3, Appli
24	125.8	24.1	485	1	US-07-989-845-29	Sequence 29, Appl
25	125.8	24.1	485	1	US-07-989-844-13	Sequence 13, Appl
26	125.8	24.1	485	1	US-08-110-663-1	Sequence 1, Appli
27	125.8	24.1	485	1	US-08-169-688-1	Sequence 1, Appli
28	125.8	24.1	485	1	US-08-240-121-13	Sequence 13, Appl
29	125.8	24.1	485	1	US-08-451-241-13	Sequence 13, Appl
30	125.8	24.1	485	1	US-08-110-664-1	Sequence 1, Appli
31	125.8	24.1	485	1	US-08-446-882-1	Sequence 1, Appli
32	125.8	24.1	485	1	US-08-385-187A-1	Sequence 1, Appli
33	125.8	24.1	485	1	US-08-470-108-1	Sequence 1, Appli
34	125.8	24.1	485	5	PCT-US93-11297-13	Sequence 13, Appl
35	125.8	24.1	485	5	PCT-US93-11298-29	Sequence 29, Appl
36	125.6	24.0	243	2	US-08-482-182-75	Sequence 75, Appl
37	124.2	23.7	717	1	US-08-284-784-40	Sequence 40, Appl
38	124.2	23.7	717	2	US-08-854-811-40	Sequence 40, Appl
39	124.2	23.7	783	1	US-08-284-784-43	Sequence 43, Appl
40	124.2	23.7	783	2	US-08-854-811-43	Sequence 43, Appl
41	124.2	23.7	891	1	US-08-284-784-33	Sequence 33, Appl
42	124.2	23.7	891	1	US-08-284-784-34	Sequence 34, Appl
43	124.2	23.7	891	2	US-08-854-811-33	Sequence 33, Appl
44	124.2	23.7	891	2	US-08-854-811-34	Sequence 34, Appl
45	124.2	23.7	900	1	US-08-284-784-24	Sequence 24, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-142-583A-3

; Sequence 3, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible



Db 331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

QY 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420  
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Db 391 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 450  
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QY 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480  
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Db 451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510  
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QY 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523  
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Db 511 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 553

RESULT 2

US-09-142-583A-5

; Sequence 5, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/142,583A

; FILING DATE: 29-Oct-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB97/00658

; FILING DATE: 11-MAR-1997

; APPLICATION NUMBER: GB 9605124.8

; FILING DATE: 11-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B. J.

; REGISTRATION NUMBER: 36663

; REFERENCE/DOCKET NUMBER: 117-263

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 7038164000

; TELEFAX: 7038164100

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 553 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

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;      MOLECULE TYPE: cDNA
;      FEATURE:
;          NAME/KEY: CDS
;          LOCATION: 341..397
;      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-142-583A-5

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Query Match          100.0%;  Score 523;  DB 3;  Length 553;
Best Local Similarity 100.0%;  Pred. No. 1.6e-154;
Matches 523;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      31  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy     61  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        |||
Db     91  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        |||
Db    151  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
        |||
Db    211  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 270

Qy    241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        |||
Db    271  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy    301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA 360
        |||
Db    331  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA 390

Qy    361  CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
        |||
Db    391  CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 450

Qy    421  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
        |||
Db    451  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy    481  CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
        |||
Db    511  CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 553

```

# RESULT 3

US-09-142-583A-10

; Sequence 10, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:



; ADDRESSEE: NIXON & VANDERHYE P.C.  
 ; STREET: 1100 NORTH GLEBE ROAD  
 ; CITY: ARLINGTON  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22201  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/142,583A  
 ; FILING DATE: 29-Oct-1998  
 ; CLASSIFICATION: <Unknown>  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/GB97/00658  
 ; FILING DATE: 11-MAR-1997  
 ; APPLICATION NUMBER: GB 9605124.8  
 ; FILING DATE: 11-MAR-1996  
 ;  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: SADOFF, B. J.  
 ; REGISTRATION NUMBER: 36663  
 ; REFERENCE/DOCKET NUMBER: 117-263  
 ;  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 7038164000  
 ; TELEFAX: 7038164100  
 ;  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 777 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ;  
 ; MOLECULE TYPE: cDNA  
 ;  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 26..493  
 ;  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
 US-09-142-583A-10

Query Match 63.6%; Score 332.8; DB 3; Length 777;  
 Best Local Similarity 84.4%; Pred. No. 9.8e-95;  
 Matches 444; Conservative 0; Mismatches 27; Indels 55; Gaps 4;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	179	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	238
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	239	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	298
Qy	121	ACAGGCATCGTGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	299	ACAGGTATCGTGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	358
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240

Db	359	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	418
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	419	ATGCCCAAGACCCAG-----	433
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	434	-----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA	486
Qy	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	487	CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG	546
Qy	421	CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT	478
Db	547	CTCTGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT	606
Qy	479	TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC	523
Db	607	TTAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC	652

5405942-2

APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,  
JAMES P.  
TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS  
I AND II

;  
CURRENT APPLICATION DATA:

FILING DATE: 16-JUN-1987

APPLICATION NUMBER: 630,557

;SEO ID NO:2:

5405942-2

Matches 359; Conservative 84; Mismatches 28; Indels 55; Gaps 4;

Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240  
 :| |||||:||||| || ||| ||| |||:| |:|:||||| ||||| |||||  
 Db 225 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGUCUGUCCGUGCCAGCGCCACACCGAC 284  
 Qy 241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300  
 |:||||| |||  
 Db 285 AUGCCCAAGACCCAG----- 299  
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360  
 |||||:||||:||||| ||||:|||||:||||| |||||:|  
 Db 300 -----AAGGAAGUACAUUUGAAGAACGCAAGUAGAGGGAGUGCAGGAAACAAGAACUA 352  
 Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420  
 ||||:|:|||||: |:|||||:|||| |||| ||||| ||||| ||::|  
 Db 353 CAGGAUGUAGGAAGACCCUCCUGAGGAGUGAAGAGUGACAUGCCACCGCAGGAUCCUUG 412  
 Qy 421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTTGATCACAT 478  
 |:|:|||| |:|:|||| |:|:|:| ||| |||||:|:|:|:| |:|:|  
 Db 413 CUCUGCACGAGUUACCUGUUAACUUUGGAACACCUACCAAAAAUAAGUUUGAUAACAU 472  
 Qy 479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523  
 :: ||||: ||| ::|:|||||:||||:|||||:||||:|  
 Db 473 UUAAGAAGUGGCGUUUCCCCCAAUGAAAUACACAAGUAAACAUUC 518

RESULT 5

US-08-472-809B-8

; Sequence 8, Application US/08472809B

; Patent No. 5925564

; GENERAL INFORMATION:

; APPLICANT: Schwartz, Robert J.

; APPLICANT: DeMayo, Franco J.

; APPLICANT: O'Malley, Bert W.

; TITLE OF INVENTION: Expression Vector Systems and

; TITLE OF INVENTION: Method of Use

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,809B

; FILING DATE: June 7, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/209,846

; FILING DATE: March 9, 1994  
 ; APPLICATION NUMBER: 07/789,919  
 ; FILING DATE: No. 5925564ember 6, 1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 214/212  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5707 bases  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 US-08-472-809B-8

Query Match 52.5%; Score 274.6; DB 2; Length 5707;  
 Best Local Similarity 82.2%; Pred. No. 5.3e-76;  
 Matches 351; Conservative 0; Mismatches 24; Indels 52; Gaps 1;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      793 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 852

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      853 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 912

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      913 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 972

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      |||
Db      973 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 1032

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      1033 ATGCCCAAGACCCAG----- 1047

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      1048 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 1100

Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db      1101 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 1160

Qy      421 CTCTGCA 427
      |||
Db      1161 GGCTGCA 1167

```

RESULT 6

US-08-472-809B-7

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; Sequence 7, Application US/08472809B
; Patent No. 5925564
; GENERAL INFORMATION:
;   APPLICANT: Schwartz, Robert J.
;   APPLICANT: DeMayo, Franco J.
;   APPLICANT: O'Malley, Bert W.
;   TITLE OF INVENTION: Expression Vector Systems and
;   TITLE OF INVENTION: Method of Use
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Lyon & Lyon
;     STREET: 633 West Fifth Street
;     STREET: Suite 4700
;     CITY: Los Angeles
;     STATE: California
;     COUNTRY: U.S.A.
;     ZIP: 90071-2066
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;     MEDIUM TYPE: storage
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: IBM P.C. DOS 5.0
;     SOFTWARE: Word Perfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/472,809B
;     FILING DATE: June 7, 1995
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/209,846
;     FILING DATE: March 9, 1994
;     APPLICATION NUMBER: 07/789,919
;     FILING DATE: No. 5925564ember 6, 1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Warburg, Richard J.
;     REGISTRATION NUMBER: 32,327
;     REFERENCE/DOCKET NUMBER: 214/212
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (213) 489-1600
;     TELEFAX: (213) 955-0440
;     TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 6345 bases
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
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US-08-472-809B-7

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Query Match          52.5%; Score 274.6; DB 2; Length 6345;
Best Local Similarity 82.2%; Pred. No. 5.6e-76;
Matches 351; Conservative 0; Mismatches 24; Indels 52; Gaps 1;
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```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||||||||||||||| ||||||||||||||||||||||||||||||||
```

```

Db      3702 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 3761
Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      3762 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 3821
Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      3822 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 3881
Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      3882 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 3941
Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      3942 ATGCCCAAGACCCAG----- 3956
Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      3957 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 4009
Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db      4010 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 4069
Qy      421 CTCTGCA 427
      |||
Db      4070 GGCTGCA 4076

```

RESULT 7

5405942-13

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,  
;JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS  
;I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:13:

; LENGTH: 357

5405942-13

Query Match 44.8%; Score 234.4; DB 6; Length 357;

Best Local Similarity 93.8%; Pred. No. 5.1e-64;

Matches 244; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      43 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 102

```

```

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      103 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 162

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      163 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 222

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      223 TGCGCACCCCTCAGGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 282

Qy      241 ATGCCCAAGACTCAGAAGTA 260
      |||
Db      283 ATGCCCAAGACCCAGAAGGA 302

```

RESULT 8

5405942-9

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,  
; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS  
; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:9:

; LENGTH: 357

5405942-9

Query Match 44.5%; Score 232.8; DB 6; Length 357;  
Best Local Similarity 76.5%; Pred. No. 1.6e-63;  
Matches 199; Conservative 44; Mismatches 17; Indels 0; Gaps 0;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
      |||
Db      43 GGACCGGAGACGCUCUGCGGGGUGAGCUGGUGGACGCUCUUCAGUUCGUGUGUGGAGAC 102

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      103 AGGGGCUUUUAUUUCAACAAGCCACAGGGUAUGGCUCACAGUCGGAGGGCGCCUCAG 162

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      163 ACAGGUAUCGUGGAUGAGUGCUGUUUCCGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 222

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      :|
Db      223 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGUCUGUCCGUGGCCAGCGCCACACCGAC 282

Qy      241 ATGCCCAAGACTCAGAAGTA 260
      |:|

```

Db 283 AUGCCCAAGACCCAGAAGGA 302

RESULT 9

5405942-7

;Patent No. 5405942  
; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,  
;JAMES P.  
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS  
;I AND II  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/65,673  
; FILING DATE: 16-JUN-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 630,557  
; FILING DATE: 19-JUL-1984  
;SEQ ID NO:7:  
; LENGTH: 210  
5405942-7

Query Match 36.6%; Score 191.4; DB 6; Length 210;  
Best Local Similarity 75.1%; Pred. No. 1.2e-50;  
Matches 157; Conservative 41; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60  
| | | | | | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 1 GGACCGGAGACGCUCUGCGGGGUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60  
  
Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120  
| | | | | : : : : : | : | | | | | | | | | | : | | | | | : | | | | | : | | | | |  
Db 61 AGGGGCUUUUAUUAACAAGCCACAGGGUAUGGCUCAGCAGUCGGAGGGCGCCUCAG 120  
  
Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 121 ACAGGUAUCGUGGAUGAGUGCGUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180  
  
Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209  
: | | | | | : | | | | | | | | | | | | | | | |  
Db 181 UGCGCACCCCUCAAGCCUGCCAAGUCAGC 209

RESULT 10

5405942-11

;Patent No. 5405942  
; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,  
;JAMES P.  
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS  
;I AND II  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/65,673  
; FILING DATE: 16-JUN-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 630,557  
; FILING DATE: 19-JUL-1984  
;SEQ ID NO:11:



; LENGTH: 210  
5405942-11

Query Match 36.6%; Score 191.4; DB 6; Length 210;  
Best Local Similarity 94.7%; Pred. No. 1.2e-50;  
Matches 198; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||
Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        |||
Db    121 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
        ||
Db    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 209
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RESULT 11

US-09-255-829-13

; Sequence 13, Application US/09255829

; Patent No. 6461617

; GENERAL INFORMATION:

; APPLICANT: Shone, Clifford Charles

; APPLICANT: Quinn, Conrad Padraig

; APPLICANT: Foster, Keith Alan

; TITLE OF INVENTION: Recombinant Toxin Fragments

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/255,829

; FILING DATE: 23-FEB-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB97/02273

; FILING DATE: 22-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/782,893

; FILING DATE: 27-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: ESMOND, ROBERT W.

```

;     REGISTRATION NUMBER: 32,893
;     REFERENCE/DOCKET NUMBER: 1581.0130002
;     TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202-371-2600
;     TELEFAX: 202-371-2540
;     INFORMATION FOR SEQ ID NO: 13:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 2862 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..2862
US-09-255-829-13

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Query Match          36.6%; Score 191.4; DB 4; Length 2862;
Best Local Similarity 94.7%; Pred. No. 4.8e-50;
Matches 198; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2644 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 2703

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
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Db      2704 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 2763

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db      2764 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 2823

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
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Db      2824 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 2852

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RESULT 12
5405942-15
;Patent No. 5405942
;  APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;  TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;  NUMBER OF SEQUENCES: 16
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/07/65,673
;  FILING DATE: 16-JUN-1987
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 630,557
;  FILING DATE: 19-JUL-1984
;SEQ ID NO:15:
;  LENGTH: 210
5405942-15

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Query Match          36.3%; Score 189.8; DB 6; Length 210;

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; REFERENCE/DOCKET NUMBER: 51875
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232
US-08-308-196A-1

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Query Match          35.4%; Score 185.2; DB 1; Length 240;
Best Local Similarity 91.6%; Pred. No. 1.1e-48;
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
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Db      77 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 136
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Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        |||
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Db      197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230
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#### RESULT 14

PCT-US91-06452-1

; Sequence 1, Application PC/TUS9106452

#### ; GENERAL INFORMATION:

; APPLICANT: Brierley, Russell A.

; APPLICANT: Davis, Geneva R.

; APPLICANT: Holtz, Gregory C.

; APPLICANT: Gleeson, Martin A.

; APPLICANT: Bradley, D. H.

; TITLE OF INVENTION: Production of Insulin-Like Growth

; TITLE OF INVENTION: Factor-1 in Methyloleophilic Yeast Cells

; NUMBER OF SEQUENCES: 12

#### ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fitch, Even, Tabin & Flannery

; STREET: 135 South LaSalle Street, Suite 900

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/06452
; FILING DATE: 19910409
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/578,728
; FILING DATE: 04-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 51874
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232
PCT-US91-06452-1

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Query Match          35.4%; Score 185.2; DB 5; Length 240;
Best Local Similarity 91.6%; Pred. No. 1.1e-48;
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      17 GGACCGGAGACGCTCTGCGGGGCTGAGCTCGTGGATGCTCTGCAGTTCGTGTGTGGAGAC 76
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Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
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      |||

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      137 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 196
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Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
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Db      197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230
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RESULT 15

US-09-029-267-13

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; Sequence 13, Application US/09029267
; Patent No. 6107057
; GENERAL INFORMATION:
; APPLICANT: Crawford, Kenneth

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; APPLICANT: Zaror, Isabel  
 ; APPLICANT: Innis, Michael  
 ; TITLE OF INVENTION: Pichia Secretary Leader for Protein  
 ; TITLE OF INVENTION: Expression  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Chiron Corporation  
 ; STREET: 4560 Horton Street  
 ; CITY: Emeryville  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94608  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/029,267  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Chung, Ling-Fong  
 ; REGISTRATION NUMBER: 36,482  
 ; REFERENCE/DOCKET NUMBER: 1165.100  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (510) 601-2704  
 ; TELEFAX: (510) 655-3542  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 390 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; DESCRIPTION: /desc = "Synthetic"  
 US-09-029-267-13

Query Match 35.4%; Score 185.2; DB 3; Length 390;  
 Best Local Similarity 91.6%; Pred. No. 1.5e-48;  
 Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db      280 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 339

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
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Db      340 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 373
  
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Job time : 49.3585 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:29:55 ; Search time 233.512 Seconds  
(without alignments)  
7443.919 Million cell updates/sec

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Perfect score: 523  
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		%				
		Query				



1	523	100.0	523	9	US-09-852-261-5	Sequence 5, Appli
2	467.4	89.4	517	9	US-09-852-261-1	Sequence 1, Appli
3	409	78.2	471	9	US-09-852-261-13	Sequence 13, Appl
4	356.8	68.2	539	9	US-09-852-261-3	Sequence 3, Appli
5	349.4	66.8	651	15	US-10-161-088-1	Sequence 1, Appli
6	334.4	63.9	7260	10	US-09-919-497-24	Sequence 24, Appl
7	334.4	63.9	7260	10	US-09-880-107-3739	Sequence 3739, Ap
8	334.4	63.9	7260	13	US-09-873-319-707	Sequence 707, App
9	334.4	63.9	7260	13	US-09-960-706-1066	Sequence 1066, Ap
10	334.4	63.9	7260	15	US-10-136-639-4	Sequence 4, Appli
11	332.8	63.6	725	15	US-10-207-655-54	Sequence 54, Appl
12	273.6	52.3	612	13	US-10-251-661-7	Sequence 7, Appli
13	262	50.1	487	9	US-09-852-261-11	Sequence 11, Appl
14	237.6	45.4	318	9	US-09-852-261-9	Sequence 9, Appli
15	228	43.6	462	15	US-10-238-114-1	Sequence 1, Appli
16	209	40.0	286	15	US-10-161-088-3	Sequence 3, Appli
17	193	36.9	210	13	US-09-807-742-18	Sequence 18, Appl
18	191.4	36.6	2862	13	US-10-241-596-13	Sequence 13, Appl
19	187	35.8	4532	10	US-09-930-377B-1	Sequence 1, Appli
20	186.6	35.7	210	10	US-09-930-377B-2	Sequence 2, Appli
21	185.2	35.4	390	15	US-10-179-046-13	Sequence 13, Appl
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23	162.8	31.1	182	13	US-10-029-386-18231	Sequence 18231, A
24	141.6	27.1	213	15	US-10-076-816-9	Sequence 9, Appli
25	141.6	27.1	213	15	US-10-077-381-9	Sequence 9, Appli
26	127	24.3	621	9	US-09-921-398-40	Sequence 40, Appl
27	127	24.3	621	15	US-10-280-826-40	Sequence 40, Appl
28	113.4	21.7	480	9	US-09-921-398-38	Sequence 38, Appl
29	113.4	21.7	480	15	US-10-280-826-38	Sequence 38, Appl
30	101.8	19.5	210	13	US-09-807-742-19	Sequence 19, Appl
31	77.2	14.8	854	10	US-09-954-531-989	Sequence 989, App
c 32	75.4	14.4	447	9	US-09-922-217-917	Sequence 917, App
c 33	75.4	14.4	447	10	US-09-833-263-917	Sequence 917, App
c 34	75.4	14.4	447	14	US-10-025-380-917	Sequence 917, App
c 35	75.2	14.4	437	15	US-10-066-543-663	Sequence 663, App
c 36	75.2	14.4	493	15	US-10-066-543-997	Sequence 997, App
c 37	75.2	14.4	518	15	US-10-066-543-1040	Sequence 1040, Ap
c 38	75.2	14.4	536	15	US-10-066-543-428	Sequence 428, App
39	75.2	14.4	543	15	US-10-136-841-1	Sequence 1, Appli
c 40	75.2	14.4	549	15	US-10-066-543-478	Sequence 478, App
c 41	75.2	14.4	574	9	US-09-922-217-918	Sequence 918, App
c 42	75.2	14.4	574	10	US-09-833-263-918	Sequence 918, App
c 43	75.2	14.4	574	14	US-10-025-380-918	Sequence 918, App
c 44	75.2	14.4	577	15	US-10-066-543-1137	Sequence 1137, Ap
c 45	75.2	14.4	579	15	US-10-066-543-1094	Sequence 1094, Ap

#### ALIGNMENTS

#### RESULT 1

US-09-852-261-5

; Sequence 5, Application US/09852261

; Patent No. US20020083477A1

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

```
; APPLICANT:  TERENGHI, GIORGIO
; TITLE OF INVENTION:  REPAIR OF NERVE DAMAGE
; FILE REFERENCE:  117-351
; CURRENT APPLICATION NUMBER:  US/09/852,261
; CURRENT FILING DATE:  2001-05-10
; PRIOR APPLICATION NUMBER:  GB 0011278.9
; PRIOR FILING DATE:  2000-05-10
; NUMBER OF SEQ ID NOS:  14
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH:  523
;   TYPE:  DNA
;   ORGANISM:  Oryctolagus cuniculus
US-09-852-261-5
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Query Match          100.0%;  Score 523;  DB 9;  Length 523;
Best Local Similarity 100.0%;  Pred. No. 1.9e-161;
Matches 523;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61  AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db     61  AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy    241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy    301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy    361  CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
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Db    361  CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420

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RESULT 2

US-09-852-261-1  
; Sequence 1, Application US/09852261  
; Patent No. US20020083477A1  
; GENERAL INFORMATION:  
; APPLICANT: GOLDSPIK, GEOFFREY  
; APPLICANT: TERENCE, GIORGIO  
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE  
; FILE REFERENCE: 117-351  
; CURRENT APPLICATION NUMBER: US/09/852,261  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: GB 0011278.9  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 517  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-852-261-1

Query Match 89.4%; Score 467.4; DB 9; Length 517;  
Best Local Similarity 96.2%; Pred. No. 3.8e-143;  
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	61	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240
Db	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G	297
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	298	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Qy	361	CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG	420
Db	358	CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG	416
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT	480
Db	417	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT	476
Qy	481	CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT	521



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Qy      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Db      369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy      481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
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RESULT 4

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US-09-852-261-3
; Sequence 3, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-852-261-3

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Query Match          68.2%; Score 356.8; DB 9; Length 539;
Best Local Similarity 82.3%; Pred. No. 9.9e-107;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db     61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTTCGGAGGGCACACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    121 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCATCCGGGCCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          ||||||||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCATTCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA 360
          ||||||||||| ||||||||||| ||||||||||| |||||||||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGAGGAAACAAGACCTA 360

```



Qy	241	ATGCCCAAGACTCAGAACTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	379	ATGCCCAAGACTCAGAACTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG	438
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	439	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA	498
Qy	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	499	CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCAGCAGGATCCTTTG	558
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC	474
Db	559	CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA	618
Qy	475	ACATTTTCAAAGAT-GGCATTTCCCCCAATGAAA	506
Db	619	ACATTACAAAGATGGGCATTTCCCCCAATGAAA	651

US-09-919-497-24

; Patent No. US20020106662A1

: GENERAL INFORMATION:

; APPLICANT: Mutter, George L.

10 TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

; FILE REFERENCE: B0801/7225

; CURRENT APPLICATION NUMBER: US/09/919,497

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/221,735

; PRIOR FILING DATE: 2000-07-31

; NUMBER OF SEQ ID NOS: 100

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; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 24

; LENGTH: 7260

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-919-497-24

Query Match 63.9%; Score 334.4; DB 10; Length 7260;

Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	311	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	370
Qy	61	AGGGGCTTTTATTTCACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	371	AGGGGCTTTTATTTCACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	430
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	431	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490

```

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      || |||||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||||
Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420
      |||||
Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||||
Db      679 CTCTGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      || |||||
Db      739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784

```

# RESULT 7

US-09-880-107-3739

```

; Sequence 3739, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3739
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025
US-09-880-107-3739

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Query Match          63.9%; Score 334.4; DB 10; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```



Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60  
 |||  
 Db 311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370  
 Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120  
 |||  
 Db 371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430  
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180  
 |||  
 Db 431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490  
 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240  
 |||  
 Db 491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550  
 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300  
 |||  
 Db 551 ATGCCCAAGACCCAG----- 565  
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360  
 |||  
 Db 566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618  
 Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420  
 |||  
 Db 619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678  
 Qy 421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478  
 |||  
 Db 679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738  
 Qy 479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523  
 |||  
 Db 739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784

# RESULT 8

US-09-873-319-707

; Sequence 707, Application US/09873319A

; Publication No. US20030134324A1

; GENERAL INFORMATION:

; APPLICANT: Munger, William E.

; APPLICANT: Kulkarni, Prakash

; APPLICANT: Getzenberg, Robert H.

; APPLICANT: Waga, Iwao

; APPLICANT: Yamamoto, Jun

; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic

; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles

; FILE REFERENCE: 44921-5029-US

; CURRENT APPLICATION NUMBER: US/09/873,319A

; CURRENT FILING DATE: 2001-06-05

; EARLIER APPLICATION NUMBER: US 60/223,323

; EARLIER FILING DATE: 2000-08-07

; NUMBER OF SEQ ID NOS: 755

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 707

; LENGTH: 7260  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 X57025  
US-09-873-319-707

Query Match 63.9%; Score 334.4; DB 13; Length 7260;  
Best Local Similarity 84.6%; Pred. No. 9e-99;  
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        |||
Db      371 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy      121 ACAGGCATCGTGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        |||
Db      431 ACAGGCATCGTGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
        |||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy      241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        |||
Db      551 ATGCCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        |||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
        |||
Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
        |||
Db      679 CTCTGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
        |||
Db      739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
```

RESULT 9

US-09-960-706-1066

; Sequence 1066, Application US/09960706

; Publication No. US20030134280A1

; GENERAL INFORMATION:

; APPLICANT: Munger, William E.

; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia Using

; TITLE OF INVENTION: Gene Expression Profiles

```
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1066
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X57025
US-09-960-706-1066
```

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Query Match          63.9%; Score 334.4; DB 13; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;
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```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db      679 CTCTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db      739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784
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RESULT 10

US-10-136-639-4

; Sequence 4, Application US/10136639

; Publication No. US20030072761A1

; GENERAL INFORMATION:

; APPLICANT: LeBowitz, Jonathan

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS THE BLOOD BRAIN

; TITLE OF INVENTION: BARRIER

; FILE REFERENCE: SYM-008

; CURRENT APPLICATION NUMBER: US/10/136,639

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 60/329,650

; PRIOR FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 7260

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-136-639-4

Query Match 63.9%; Score 334.4; DB 15; Length 7260;

Best Local Similarity 84.6%; Pred. No. 9e-99;

Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
          |||
Db      371 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
          ||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||
Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          |||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
          |||
Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
          |||

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[illegible]

RESULT 11

US-10-207-655-54

; Sequence 54, Application US/10207655

; Publication No. US20030118592A1

; GENERAL INFORMATION:

; APPLICANT: Ledbetter, Jeffrey A.

; APPLICANT: Hayden-Ledbetter, Martha S.

TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS

FILE REFERENCE: 390069.401C1

; CURRENT APPLICATION NUMBER: US/10/207,655

; CURRENT FILING DATE: 2002-07-25

; NUMBER OF SEO ID NOS: 426

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; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 54

LENGTH: 725

TYPE: DNA

; ORGANISM: Homo sapiens

US-10-207-655-54

Query Match 63.6%; Score 332.8; DB 15; Length 725;

Best Local Similarity . 84.4%; Pred. No. 9.2e-99;

Matches 444; Conservative 0; Mismatches 27; Indels 55; Gaps 4;

[illegible]

Db

Qy

Db

Qy

Dlc

Qy

Dk

Qy

Dk

Qy

Dk

Qy

De



```

Qy      241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||||
Db      487 ATGCCCCAAGACCCAG----- 501

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          |||||
Db      502 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 554

Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTT 418
          |||||
Db      555 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTT 612

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# RESULT 13

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US-09-852-261-11
; Sequence 11, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-852-261-11

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Query Match          50.1%; Score 262; DB 9; Length 487;
Best Local Similarity 74.7%; Pred. No. 1.5e-75;
Matches 396; Conservative 0; Mismatches 75; Indels 59; Gaps 3;

```

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Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||||
Db      1  GGACCGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy      61  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCCGAGGGGCACCTCAG 120
          |||||
Db      61  AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTCCGAGGGGCACCACAG 120

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||||
Db      121 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
          |||||
Db      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy      241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||||
Db      241 ATGCCCCAAGACTCAG----- 255

```





```

Db      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
Qy      241 ATGCCCAAGACTCAGAAGTA 260
        |||||
Db      241 ATGCCCAAGACCCAGAAGGA 260

```

RESULT 15

US-10-238-114-1

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; Sequence 1, Application US/10238114
; Publication No. US20030100073A1
; GENERAL INFORMATION:
; APPLICANT: Merial
; APPLICANT: ANDREONI , Christine Michele
; TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST
FELINE RETROVIRUS
; FILE REFERENCE: 454313-3165.1
; CURRENT APPLICATION NUMBER: US/10/238,114
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: FR 01 11736
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/318,666
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Felis catus
US-10-238-114-1

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```

Query Match          43.6%; Score 228; DB 15; Length 462;
Best Local Similarity 92.3%; Pred. No. 2.3e-64;
Matches 240; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||||
Db      145 GGACCAGAGACGCTCTGTGGGGCTGAGTTGGTGGACGCTCTTCAGTTCGTGTGTGGAGAC 204

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        |||||
Db      205 AGGGGTTTTATTTCAACAAGCCACGGGGTATGGCTCCAGCAGTCGGAGGGCACCTCAG 264

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        |||||
Db      265 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGCGGCTAGAGATGTAC 324

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
        |||||
Db      325 TGTGCACCCCTCAAGCCTGCCAAGTCTGCCCGCTCAGTCCGTGCTCAGCGCCACACTGAC 384

Qy      241 ATGCCCAAGACTCAGAAGTA 260
        |||||
Db      385 ATGCCCAAGGCTCAGAAGGA 404

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Search completed: December 13, 2003, 11:56:48

Job time : 235.512 secs